



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 121508**

**TO: Jennifer Graser**  
**Location: rem/3b09/3c18**  
**Art Unit: 1645**  
**Monday, May 10, 2004**

**Case Serial Number: 10/625221**

**From: Edward Hart**  
**Location: Biotech-Chem Library**  
**REM-1A55**  
**Phone: 571-272-2512**

**[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)**

### **Search Notes**

Examiner Graser,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 12:05:23 ; Search time 21 Seconds  
(without alignments)  
1012.301 Million cell updates/sec

Title: US-10-625-221-14

Perfect score: 1178  
Sequence: 1 QODPDSQLHRSSLVKNLQN.....KDNETLDSNTSQIEVYLTK 221

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:  
1: Piri:  
2: pir2:  
3: pir3:  
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1169	99.2	251	1 S28659	exotoxin type A pr
2	1133	96.2	236	2 S18783	exotoxin type A pr
3	1128	95.8	236	2 S18786	exotoxin type A pr
4	1025	87.0	236	2 S18789	exotoxin A precurs
5	978.5	83.1	250	1 A26152	streptococcal pyro
6	572	48.6	266	1 EN8AB6	enterotoxin B prec
7	546	46.3	266	2 S11885	enterotoxin C3 - S
8	543	46.1	266	2 A60114	enterotoxin C-2 pr
9	542	46.0	266	1 ENSAC1	enterotoxin C-1 pr
10	468	39.7	258	2 G89968	extracellular ente
11	337	28.6	136	2 A89969	enterotoxin YENT2
12	333.5	28.3	258	2 A33953	enterotoxin D prec
13	323.5	27.5	260	2 E89969	enterotoxin SeO (i
14	315.5	26.8	260	2 C89984	enterotoxin p (imp
15	297.5	25.3	258	2 H89968	enterotoxin SeN (i
16	293.5	24.9	257	2 A28664	enterotoxin E prec
17	291.5	24.7	257	2 A28179	extracellular ente
18	284	24.1	240	2 G89991	enterotoxin SM (i
19	265.5	22.5	239	2 D89969	extracellular ente
20	229.5	19.5	242	2 C89969	exotoxin C precurs
21	205	17.4	235	2 A30509	exotoxin Yent1
22	173	14.7	133	2 B89969	exotoxin 11 (impor
23	127	10.8	231	2 D89807	hypothetical prote
24	123.5	10.5	157	2 A89942	exotoxin 15 (impor
25	123	10.4	227	2 C89808	exotoxin 9 (impor
26	114	9.7	292	2 B89807	exotoxin 10 (impor
27	112.5	9.6	234	2 C89807	hypothetical prote
28	109.5	9.3	1367	2 T18466	exotoxin 13 (impor
29	105.5	9.0	232	2 F89807	

30 105.5 9.0 596 2 E96935 FUSION, methionine  
31 105.5 9.0 825 2 H82885 hypothetical prote  
32 102 8.7 1856 2 C95008 immunoglobulin A1  
33 101 8.6 234 1 XC8AS1 toxic shock syndro  
34 101 8.6 770 2 B48910 desmocolin 1a pre  
35 101 8.6 824 2 A48910 desmocolin 1a pre  
36 101 8.6 840 2 I37281 Dscia precursor -  
37 101 8.6 894 2 I37282 Dscib precursor -  
38 100 8.5 4981 2 T18489 hypothetical prote  
39 98 8.3 234 2 B89992 toxic shock syndro  
40 98 8.3 433 2 G90604 hypothetical prote  
41 97.5 8.3 463 2 D95019 hypothetical prote  
42 96 8.1 241 2 B89888 hypothetical prote  
43 96 8.1 336 2 S09627 prrc protein - Esc  
44 96 8.1 908 2 C70168 DNA polymerase I (  
45 96 8.1 1306 2 T28313 ORF MSV152 probabl

ALIGNMENTS

RESULT 1  
S29659  
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12  
N:Alternate names: erythrogenic toxin; scarlet fever toxin  
C:Species: Streptococcus pyogenes phage T12  
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999  
C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800  
R:Weeks, C.R.; Ferretti, J.J.  
Infect. Immun. 52, 144-150, 1986  
A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) g  
A:Reference number: S29659; MUID:86166804; PMID:3514452  
A:Accession: S29659  
A:Molecule type: DNA  
A:Residues: 1-251 <WEB>  
R:Cross-references: EMBL:U0453; EMBL:M19350; NID:G1877426; PIDN:AAC48868.1; PID:G1877430  
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.  
J. Exp. Med. 174, 1271-1274, 1991  
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod  
A:Reference number: S18782; MUID:92044323; PMID:1940804  
A:Accession: S18782  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NEB>  
A:Cross-references: EMBL:X61560; NID:G47287; PIDN:CAA43758.1; PID:G47288  
A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18784  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NEA>  
A:Cross-references: EMBL:X61556; NID:G47291; PIDN:CAA43754.1; PID:G47292  
A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18785  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NEZ>  
A:Cross-references: EMBL:X61559; NID:G47293; PIDN:CAA43757.1; PID:G47294  
A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned ph  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18791  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NEY>  
A:Cross-references: EMBL:X61555; NID:G47309; PIDN:CAA43753.1; PID:G47310  
A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18796  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 9-244 <NEO>  
A:Cross-references: EMBL:X61557; NID:G47319; PIDN:CAA43755.1; PID:G47320

A;Residues: 1-236 <NEZ>  
A;Cross-references: EMBL:X61570; NID:g47315; PIDN:CRA43768.1; PID:g47316  
A;Experimental source: strain MGAS491 isolate United Kingdom unassigned phase  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18801  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-236 <NEY>  
A;Cross-references: EMBL:X61572; NID:g47333; PIDN:CRA43770.1; PID:g47334  
A;Experimental source: strain MGAS654 isolate Germany unassigned phase  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18798  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-236 <NEO>  
A;Cross-references: EMBL:X61571; NID:g47323; PIDN:CRA43769.1; PID:g47324  
A;Experimental source: strain MGAS495 isolate Germany unassigned phase  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
C;Genetics:  
C;Gene: speA3  
C;Superfamily: enterotoxin B  
C;Keywords: exotoxin  
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>  
F;23-236/Product: exotoxin type A (fragment) #status predicted <AT>

	Query Match	96.2%; Score 1133; DB 2; Length 236;
	Best Local Similarity 99.1%; Pred. No. 2.2e-80;	
	Matches 212; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 QQPDPSPQLHRSLSKVLQNIIYFLYEGDPTVHENYKVSVDQLLSHHLLIYNVSGPNVDKLKT 60	
Dd	23 QQPDPSPQLHRSLSKVLQNIIYFLYEGDPTVHENYKVSVDQLLSHHLLIYNVSGPNVDKLKT 82	
Qy	61 ELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAESACIYGGVTNHGHNHLEIPKKIVVK 120	
Dd	83 ELKNQEMATLFKDKNIDIYGVEYYHLCYLCENAESACIYGGVTNHGHNHLEIPKKIVVK 142	
Qy	121 VSDIGTQSISFDIETNKQWVAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPOKKE 180	
Dd	143 VSDIGTQSISFDIETNKQWVAQELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPOKKE 202	
Qy	181 SFWFDFPPEFTQSKYLMIYKDNETLDSNTSQI 214	
Dd	203 SFWFDFPPEFTQSKYLMIYKDNETLDSNTSQI 236	

RESULT 3  
S18786  
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isolate)  
N;Alternate names: scarlet fever toxin  
C;Species: Streptococcus pyogenes phage  
A;Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain  
isolate United Kingdom; strain MGAS496 isolate Germany  
C;Date: 29-Jan-1993 #sequence revision 29-Jan-1993 #text change 16-Jul-1999  
C;Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799  
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.  
J. Exp. Med. 174, 1271-1274, 1991  
A;Title: Characterization and clonal distribution of four alleles of the speA gene enc  
A;Reference number: S18782; PMID:92044323; PMID:1940804  
A;Accession: S18786  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-236 <NEL>  
A;Cross-references: EMBL:X61561; NID:g47297; PIDN:CRA43759.1; PID:g47298  
A;Experimental source: strain MGAS250 isolate California unassigned phase  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A;Accession: S18787  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-236 <NEA>  
A;Cross-references: EMBL:X61562; NID:g47299; PIDN:CRA43760.1; PID:g47300  
A;Experimental source: strain MGAS251 isolate California unassigned phase  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991

A:Accession: S18788  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NE>  
A:Cross-references: EMBL:X61563; NID:G47301; PIDN:CAA43761.1; PID:G47302  
A:Experimental source: strain MGAS256 isolate California unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18790  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NE>  
A:Cross-references: EMBL:X61564; NID:G47305; PIDN:CAA43762.1; PID:G47306  
A:Experimental source: strain MGAS285 isolate Colorado unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18792  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NE>  
A:Cross-references: EMBL:X61565; NID:G47311; PIDN:CAA43763.1; PID:G47312  
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18795  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NE>  
A:Cross-references: EMBL:X61566; NID:G47317; PIDN:CAA43764.1; PID:G47318  
A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Accession: S18799  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NE>  
A:Cross-references: EMBL:X61567; NID:G47325; PIDN:CAA43765.1; PID:G47326  
A:Experimental source: strain MGAS496 isolate Germany unassigned phage  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Genetics:  
C:Gene: speA2  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>  
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>  
Query Match 95.8%; Score 1128; DB 2; Length 236;  
Best Local Similarity 99.1%; Pred. No. 5.4e-80; Indels 0; Gaps 0;  
Matches 212; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLIYNVSGPNYDKLKT 60  
Db 23 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYNVSGPNYDKLKT 82  
Qy 61 ELKNQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTHNHNHLEIPKIVVK 120  
Db 83 ELKNQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTHNHNHLEIPKIVVK 142  
Qy 121 VSDIGIQLSFDIETNKKVMTAQELDYKVRKYLTDNKLQYTNNGPSKYETGYIKFIPKNKE 180  
Db 143 VSDIGIQLSFDIETNKKVMTAQELDYKVRKYLTDNKLQYTNNGPSKYETGYIKFIPKNKE 202  
Qy 181 SFWDFPPEFTQSKYLMYKDNETLDSNTSQI 214  
Db 203 SFWDFPPEFTQSKYLMYKDNETLDSNTSQI 236  
Query Match 95.8%; Score 1128; DB 2; Length 236;  
Best Local Similarity 99.1%; Pred. No. 5.4e-80; Indels 0; Gaps 0;  
Matches 212; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLIYNVSGPNYDKLKT 60  
Db 23 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYNVSGPNYDKLKT 82  
Qy 61 ELKNQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTHNHNHLEIPKIVVK 120  
Db 83 ELKNQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTHNHNHLEIPKIVVK 142  
Qy 121 VSDIGIQLSFDIETNKKVMTAQELDYKVRKYLTDNKLQYTNNGPSKYETGYIKFIPKNKE 180  
Db 143 VSDIGIQLSFDIETNKKVMTAQELDYKVRKYLTDNKLQYTNNGPSKYETGYIKFIPKNKE 202  
Qy 181 SFWDFPPEFTQSKYLMYKDNETLDSNTSQI 214  
Db 203 SFWDFPPEFTQSKYLMYKDNETLDSNTSQI 236  
RESULT 4  
S18789  
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate California)  
N:Alternate names: scarlet fever toxin  
C:Species: Streptococcus pyogenes  
A:Variety: strain MGAS262 isolate California  
C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 16-Jul-1999  
C:Accession: S18789  
R:Nelson, K.; Schlievert, P.M.; Seldander, R.K.; Musser, J.M.  
J. Exp. Med. 174, 1271-1274, 1991

A:Title: Characterization and clonal distribution of four alleles of the speA gene encoded  
A:Reference number: S18782; MUID:92044323; PMID:1940804  
A:Accession: S18789  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-236 <NE>  
A:Cross-references: EMBL:X61573; NID:G47303; PIDN:CAA43771.1; PID:G47304  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991  
A:Genetics:  
C:Gene: speA  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>  
F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>  
Query Match 87.0%; Score 1025; DB 2; Length 236;  
Best Local Similarity 89.7%; Pred. No. 4.9e-72; Indels 0; Gaps 0;  
Matches 192; Conservative 12; Mismatches 10; Indels 0; Gaps 0;  
Qy 1 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLIYNVSGPNYDKLKT 60  
Db 23 QDDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYNVSGPNYDKLKT 82  
Qy 61 ELKNQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTHNHNHLEIPKIVVK 120  
Db 83 ELKNQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTHNHNHLEIPKIVVK 142  
Qy 121 VSDIGIQLSFDIETNKKVMTAQELDYKVRKYLTDNKLQYTNNGPSKYETGYIKFIPKNKE 180  
Db 143 VSDIGIQLSFDIETNKKVMTAQELDYKVRKYLTDNKLQYTNNGPSKYETGYIKFIPKNKE 202  
Qy 181 SFWDFPPEFTQSKYLMYKDNETLDSNTSQI 214  
Db 203 TFWDFPPEFTQSKYLMYKDNETLDSNTSQI 236  
RESULT 5  
A26152  
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.  
N:Alternate names: scarlet fever toxin; SPE type A (speA)  
C:Species: Streptococcus sp.  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A26152  
R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.  
Mol. Gen. Genet. 203, 354-356, 1986  
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta  
A:Reference number: A26152; MUID:86284313; PMID:3526093  
A:Accession: A26152  
A:Molecule type: DNA  
A:Residues: 1-250 <JOH>  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
Query Match 83.1%; Score 978.5; DB 1; Length 250;  
Best Local Similarity 86.7%; Pred. No. 2.1e-66; Indels 1; Gaps 1;  
Matches 189; Conservative 4; Mismatches 24; Indels 1; Gaps 1;  
Qy 4 PDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLIYNVSGPNYDKLKT 63  
Db 34 PKPSQLQRSNLVTKFKIYIFMVRVLVTHENVKSVQDQLSHDLIYNVSGPNYDKLKT 93  
Qy 64 NQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTHNHNHLEIPKIVVK 123  
Db 94 NQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTHNHNHLEIPKIVVK 153  
Qy 124 DGIQSLSFDIETNKKVMTAQELDYKVRKYLTDNKLQYTNNGPSKYETGYIKFIPKNKESFW 183  
Db 154 DGIQSLSFDIETNKKVMTAQELDYKVRKYLTDNKLQYTNNGPSKYETGYIKFIPKNKESFW 212  
Qy 184 FDFPPEFTQSKYLMYKDNETLDSNTSQI 221  
Db 213 FDFPPEFTQSKYLMYKDNETLDSNTSQI 250

## RESULT 6

enterotoxin B precursor - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C:Date: 24-Apr-1984 #sequence\_revision 15-Oct-1996 #text\_change 18-Jun-1999  
C:Accession: S27360; A92065; S27240; A01815  
R:Jones, C.L.; Khan, S.A.  
J. Bacteriol. 166, 29-33, 1986  
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.  
A:Reference number: S27360; MUID:86168029; PMID:3957869  
A:Accession: S27360  
A:Molecule type: DNA  
A:Residues: 1-266 <JON>  
A:Cross-references: EMBL:M1118; NID:gl52999; PIDN:AAA88550.1; PID:gl53000  
A:Experimental source: strain S6  
R:Huang, I.Y.; Bergdoll, M.S.  
J. Biol. Chem. 245, 3518-3525, 1970  
A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide  
A:Reference number: A92065; MUID:71007902; PMID:5470821  
A:Accession: A92065  
A:Molecule type: protein  
A:Residues: 28-55; 'NND', 59-68, 'NE', 71, 'FDLIY', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',  
A:Experimental source: strain S-6  
R:Huang, I.Y.; Bergdoll, M.S.  
J. Biol. Chem. 245, 3511-3517, 1970  
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition  
A:Reference number: A92064; MUID:71007901; PMID:5470820  
A:Contents: annotation; chymotryptic peptides  
R:Huang, I.Y.; Bergdoll, M.S.  
Biochemistry 4, 1011-1016, 1965  
A:Title: Purification of staphylococcal enterotoxin B.  
A:Reference number: A90548; MUID:66035792; PMID:4953912  
A:Contents: annotation; biological source of protein  
R:Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni  
Eur. J. Biochem. 209, 823-828, 1992  
A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B  
A:Reference number: S27240; MUID:93049338; PMID:1425690  
A:Accession: S27240  
A:Molecule type: protein  
A:Residues: 28-42; 128-148 <ALA>  
C:Superfamily: enterotoxin B  
C:Keywords: enterotoxin; extracellular protein; toxin  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-266/Product: enterotoxin B #status experimental <MAT>  
F:120-140/Disulfide bonds: #status experimental

Query Match 48.6%; Score 572; DB 1; Length 266;  
Best Local Similarity 49.2%; Pred. No. 5.6e-37;  
Matches 116; Conservative 36; Mismatches 68; Indels 16; Gaps 5;

QY 1 QDDPPSOLHSSLVKNL-QNIFYLYEGDPVTHENVKSVDDLLSHHLYNVSGP---NYD 56  
DB 30 QDDPPDLHKSSEFTGMNKKVLYDDHYVSATKVKSVDFLAHDLIYNISDKKLKNYD 89  
QY 57 KLKTELKQKQEWATLPKQKNVDIYGYEYHLCYLCNA-----ERSACIYGGVTNHE 107  
DB 90 NVRFVFNKDLADKYKVDVFGANYVYQCYFSKKTNDINSQTDKRAKTCMYGGVTEHN 149  
QY 108 GNHLIIPKKIVVKSIDGTSQISFDLETKKQVTAQELDYKVKYLTNDKQLYTNGPSKY 167  
DB 150 GNQLDKYSITVRVFEDGKNLLSDVQTNKKVTAQELDYTRHYLVKNKKLYEFNNSPY 209  
QY 168 ETGYIKFIPKKNESWFDFPFEP--EFTQSKYLMYKDNELTDSNTSQIEVLTTK 221  
DB 210 ETGYIKFI-ENENSWFYDWWPAGDKFDQSKYLMYNDKNVDSKVKIEVHLTTK 264

## RESULT 7

enterotoxin C3 - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Jul-1999  
C:Accession: S11885  
R:Hyde, C.J.; Hackett, S.P.; Bohach, G.A.  
Mol. Gen. Genet. 220, 329-333, 1990  
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compari  
A:Reference number: S11885; MUID:90220508; PMID:2325627  
A:Accession: S11885  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 1-266 <HOV>  
A:Cross-references: GB:X51661; NID:g46570; PIDN:CAA35972.1; PID:g46571  
C:Superfamily: enterotoxin B

Query Match 46.3%; Score 546; DB 2; Length 266;  
Best Local Similarity 47.2%; Pred. No. 5.7e-35;  
Matches 111; Conservative 43; Mismatches 67; Indels 14; Gaps 6;

QY 1 QDDPPSOLHSS--LVKNLQNIYFLYEGDPVTHENVKSVDDLLSHHLYNVSG---PNYD 56  
DB 30 QDDPPDDLHKSSEFTGMNKKVLYDDHYVSATKVKSVDFLAHDLIYNISDKKLKNYD 89  
QY 57 KLKTELKQKQEWATLPKQKNVDIYGYEYHLCYLC--ENAE-----SACIYGGVTNHEGNH 110  
DB 90 KVKTLLNEDLAKKYKDEVDVYGSNNYVNCYFSSKQNVGKVTGCTCMYGGITKHEGNH 149  
QY 111 LEIP--KKIVVKVSDGTSQISFDLETKKQVTAQELDYKVKYLTNDKQLYTNGPSKYE 168  
DB 150 FPNGLQNVLVRYENKNTISFEVQTDKSVTAQELDIKARFNLINKNLYEFNNSPYE 209  
QY 169 TGYIKFIPKKNESWFDFPFEP--EFTQSKYLMYKDNELTDSNTSQIEVLTTK 221  
DB 210 TGYIKFIENNGTWFYDWWPAGDKFDQSKYLMYNDKNVDSKVKIEVHLTTK 264

## RESULT 8

enterotoxin C-2 precursor - Staphylococcus aureus  
N:Alternate names: enterotoxin C-3 precursor  
C:Species: Staphylococcus aureus  
C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 16-Jul-1999  
C:Accession: A60114; B60114; A33866  
R:Bohach, G.A.; Schlievert, P.M.  
Infect. Immun. 57, 2249-2252, 1989  
A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins  
A:Reference number: A60114; MUID:89277549; PMID:2543637  
A:Accession: A60114  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-266 <BOH>  
A:Accession: B60114  
A:Molecule type: protein  
A:Residues: 28-66 <BOH2>  
R:Couch, J.L.; Betley, M.J.  
J. Bacteriol. 171, 4507-4510, 1989  
A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests th  
A:Reference number: A33866; MUID:89327174; PMID:2473979  
A:Accession: A33866  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-266 <COU>  
A:Cross-references: GB:M28364; NID:gl53003; PIDN:AAA26624.1; PID:gl53004  
C:Genetics:  
A:Gene: entC2  
C:Superfamily: enterotoxin B  
F:1-27/Domain: signal sequence #status predicted <SIG>  
F:28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 46.1%; Score 543; DB 2; Length 266;  
Best Local Similarity 46.4%; Pred. No. 9.8e-35;



Db 122 VESKINVEHLTKK 136

RESULT 12

A33953

enterotoxin D precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 15-Oct-1999

C:Accession: A33953

R;Bayles, K.W.; Iandolo, J.J.

J;Bacteriol. 171, 4799-4806, 1989

A;Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin

A;Reference number: A33953; MUID:89359112; PMID:2549000

A;Accession: A33953

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-258 <RAY>

A;Cross-references: GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g758691

C;Superfamily: enterotoxin B

Query Match 28.3%; Score 333.5; DB 2; Length 258;

Best Local Similarity 36.7%; Pred. No. 1.4e-18;

Matches 83; Conservative 42; Mismatches 86; Indels 15; Gaps 7;

QY 8 QLHR-----SSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYN---VSGPNYDKLK 59

Db 36 ELHKSELSSTALNNKHSY--ADKNPIIGENKSTGDFLENTLLYKKFFTDLLNPEDLL 93

QY 60 TELKNQEMATLFDKNVDIYGVYHLYCLENARSACIYGGVTHNHEGHNLEIPKLIIV 119

Db 94 INFNSKEMAOHFKNVDVPIRYSINCYGGE-IDRTACTYGGVTPHEGNNLKERKPIPI 152

QY 120 KVSIDGIO-SLSFD-IETNKNWVTAQELDYKVRKYLTDNKKLYTNGP--SKYETGYIKFI 175

Db 153 NLWINGVQKESVLSQVQDKVQDKNVTQELDAQARRYLQDKLXNNDTLGGIKQIKLEFD 212

QY 176 PNKESFWDFPEPFETQSKYLMYKDNETLDSNTSQTIEVLTTK 221

Db 213 SSDGSKVSYLFDVKGDFPEKQLRIYSDNKTLSLHLDIYLYEK 258

RESULT 13

E89969

enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001

C:Accession: E89969

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: E89969

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-260 <KUR>

A;Cross-references: GB:BA000018; PID:g13701623; PIDN:BAB42916.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:

A;Gene: seo

C;Superfamily: enterotoxin B

Query Match 27.5%; Score 323.5; DB 2; Length 260;

Best Local Similarity 38.5%; Pred. No. 8.6e-18;

Matches 90; Conservative 33; Mismatches 94; Indels 17; Gaps 7;

QY 1 QODPPSQLHRSGLVK--NLQNIYFLYEGDPVTHENVKSVQDQLSHHLYN---V 50

Db 30 EEDPKIESLCKSSVDPIALHNDDYINNRT--TVKSIYSTTEKFLDFLLPKSINWL 87

QY 51 SG--PNYDKLTKLNQEMATLFDKNVDIYGVYHLYCLENARSACIYGGVTHNEG 108

Db 88 DGISAFFKDLKVEFSSAISKEFLGKTVDIYGVYKAHC-GEHQVDTACTYGGVTPHEN 146

QY 109 NHLEIPKXIVVKSIDGQSISFDIETNKNWVTAQELDYKVRKYLTDNKKLYTNGPSKYE 168

Db 147 NKLSEPKNIGAVYKDNVNVNTFIVTDKKVKVTAQELDIKVRKTLNNAYKLYDRMTSDVQ 206

QY 169 TGYIKF--IPKNKESFWDFPEPFETQSKYLMYKDNETLDSNTSQTIEVLT 220

Db 207 KGYIKFHSHEKESFYIDLFIYKGNLPDQYLOIYNDNKTIDSSDYHLDVILFT 260

RESULT 14

C89984

enterotoxin P [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001

C:Accession: C89984

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: C89984

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-260 <KUR>

A;Cross-references: GB:BA000018; PID:g13701743; PIDN:BAB43036.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:

A;Gene: sep

C;Superfamily: enterotoxin B

Query Match 26.8%; Score 315.5; DB 2; Length 260;

Best Local Similarity 36.7%; Pred. No. 3.6e-17;

Matches 84; Conservative 44; Mismatches 74; Indels 27; Gaps 12;

QY 7 SOLHRSVLKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYN--VSGN-YDKLTKTELK 63

Db 43 SELQGTAL-SNLKQTYI-HNGSAII-ENKESNDQFLKNTILFNDFPTGHQWYNDLLVDLG 99

QY 64 NOEMATLFDKNVDIYGVYHLYCLENAE--RSACIYGGVTHNHEGHNLEIPKLIIVKV 121

Db 100 SSTANIYKGVKVDLYGVY---GYCTGTFPACTACMGVTLHDNNOLEBEKKVPINL 156

QY 122 SIDGIQSL--SFDIETNKNWVTAQELDYKVRKYLTDNKKLYT----NGPSKYETGYIKFI 175

Db 157 WIDGKQNTVPLGTVKTKKEVTVQELDQSRHLYHETYNLYNTDAFNG--KIQRGLIEFH 214

QY 176 PNKESFWDFPEPFETQSKY----LMYKDNETLDSNTSQTIEVLT 220

Db 215 PSSGDSGVGYDLFG----AQQVPTQLRIRYDNKNTIKSKNMHIDIYLT 259

RESULT 15

H89968

enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001

C:Accession: H89968

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: H89968

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-258 <KUR>

A;Cross-references: GB:BA000018; PID:g13701618; PIDN:BAB42911.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:  
A;Gene: sen  
C;Superfamily: enterotoxin B

Query Match 25.3%; Score 297.5; DB 2; Length 258;  
Best Local Similarity 35.8%; Pred. No. 8.6e-16;  
Matches 77; Conservative 39; Mismatches 86; Indels 13; Gaps 6;

QY	12	SSLVKNLQNIY--FLYEGDPVTHENVKSVQDLSSHLLI---YNVSGPNYDKLKTSLKNOE	66
Db	46	SSKLFNLTSYITDITWQLD---ESNKISTDQLLNNTIILKNIDISVLKTSSLKVEFNSSD	102
QY	67	MATLFKDKNDIYGVYHYHLCY-LCENABRSACIYGGVTNHEGNHLEIPKKIIVKVSIDG	125
Db	103	LANQFKGKNIDIYGLYFGNKCUGLTE--EKTSCLYGGVTIHDGNQLDEEKVIGVNVFKDG	160
QY	126	IQSLSPDIETNKKKWTQAQLDYKVRKYLTDNKOLYTNGPSKYETGYIKIIPKN--KESFW	183
Db	161	VQEGFVIKKAKVTVQELDTKVRPLENLYKYNKDTGNTQKGCIFPHSHHQDSFY	220
QY	184	FDFFPEPFTQSKYLMYKDNETLDSNTSQIEVYL	218
Db	221	YDLNVKGSVGAEEFFQFYSDNRTVSSSNVHIDVFL	255

Search completed: May 7, 2004, 12:09:40  
Job time : 22 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 7, 2004, 12:01:27 ; Search time 17 Seconds  
(without alignments)  
676.912 Million cell updates/sec

Title: US-10-625-221-14  
Perfect score: 1178  
Sequence: 1 QQDFDPSQLRSLVKNLQN.....KDNETLDSNTSQIEVYLTK 221

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1169	99.2	251	1	SPEA STRPY
2	572	48.6	266	1	ETXG STAAU
3	546	46.3	266	1	ETC3 STAAU
4	543	46.1	266	1	ETC1 STAAU
5	542	46.0	266	1	ETC1 STAAU
6	468	39.7	258	1	ETXG STAAU
7	333.5	28.3	258	1	ETXG STAAU
8	293.5	24.9	257	1	ETXG STAAU
9	291.5	24.7	257	1	ETXG STAAU
10	281.5	23.9	241	1	ETXG STAAU
11	209.5	17.8	236	1	SPEH STRPY
12	205	17.4	235	1	SPEC STRPY
13	162	13.8	234	1	SPEG STRPY
14	101	8.6	234	1	TSST STAAU
15	101	8.6	894	1	DSCI HUMAN
16	96	8.1	396	1	PRRC ECOLI
17	96	8.1	908	1	DPO1 BORBU
18	95.5	7.9	999	1	HGP2 HAEBIN
19	93	7.9	434	1	PURA WIGER
20	92	7.8	660	1	PRIA BORBU
21	91	7.7	384	1	SCST YEAAT
22	91	7.7	1956	1	ATX1 PLASTA
23	90.5	7.7	3255	1	POLG LMVE
24	90	7.6	554	1	Y478 RICPR
25	90	7.6	598	1	PRIM STAEF
26	90	7.6	3255	1	POLG LMVO
27	89.5	7.6	439	1	NADA CLOPE
28	89	7.6	968	1	RNE EUCAP
29	88.5	7.5	495	1	Y243 AQAE
30	88.5	7.5	540	1	MTAI ACTCA
31	88	7.5	181	1	RM06 ACACA
32	87.5	7.4	500	1	TACY CLOPE
33	87.5	7.4	2410	1	POLI_BAYMJ

RESULT 1

ID	SPEA STRPY	STANDARD	PRT	251 AA
AC	P08095;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Exotoxin type A precursor (Scarlet fever toxin) (Erythrocytic toxin) (SPE A).			
DE	(SPE A).			
GN	SPEA OR SPYM18_0393.			
OS	Streptococcus pyogenes, and			
OS	Streptococcus pyogenes (serotype M18).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
NCBI_TaxID	1314, 186103;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=8616804; PubMed=3514452;			
RA	Weeks C.R., Ferretti J.J.;			
RT	"Nucleotide sequence of the type A streptococcal exotoxin (erythrocytic toxin) gene from Streptococcus pyogenes bacteriophage T12.";			
RT	Infect. Immun. 52:144-150(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=8628431; PubMed=3526093;			
RT	Johnson L.P., L'Italien J.J., Schlievert P.M.;			
RT	"Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus enterotoxin B.";			
RT	Mol. Gen. Genet. 203:354-356(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	STRAIN=MGAS8232 / Serotype M18;			
RT	MEDLINE=21927593; PubMed=11917109;			
RT	Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Bares S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;			
RT	"Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).			
RA	MEDLINE=99094887; PubMed=9878045;			
RT	Papageorgiou A.C., Collins C.M., Guman D.M., Kline J.B., O'Brien S.M., Tranter H.S., Acharya K.R.;			
RT	"Structural basis for the recognition of superantigen streptococcal pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell receptors.";			
RT	EMBO J. 18:9-21(1999).			
CC	FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic fever.			
CC	!- SUBUNIT: Binds to major histocompatibility complex class II beta			

P49048 caenorhabdi  
Q91c47 arabidopsi  
Q8c2e4 oceanobaci  
P26450 mus musculu  
Q49409 mycoplasma  
P47084 saccharomyc  
Q02206 saccharomyc  
Q8d962 streptococc  
Q01107 bos taurus  
Q9kiv0 haemophilus  
P33459 caprine art  
Q04574 barley yell

chain.  
-!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.  
-!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.  
-----  
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-----  
EMBL; U0453; AAC4868.1; --  
EMBL; X03929; CAA27568.1; --  
EMBL; AB00982; AAL97141.1; --  
PIR; A26152; A26152.  
PDB; 1B1Z; 24-NOV-99.  
PDB; 1FNU; 17-NOV-00.  
PDB; 1FNV; 17-NOV-00.  
PDB; 1FNW; 17-NOV-00.  
PDB; 1HAS; 03-APR-02.  
PDB; 1LOX; 03-APR-02.  
InterPro; IPR008992; Bact\_endotox.  
InterPro; IPR006177; Bctrl\_tox.  
InterPro; IPR006123; Staph/Strep\_toxin.  
InterPro; IPR006126; Staph/Strep\_tox.  
InterPro; IPR006173; Staph\_tox\_O8.  
Pfam; PF02876; Staph\_Strep\_tox\_C7; 1.  
Pfam; PF01123; Staph\_Strep\_toxin; 1.  
PRINTS; PR00279; BACTRLTOXIN.  
PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
Toxin; Signal; 3D-structure; Complete proteome.  
FT SIGNAL 1 30 EXOTOXIN TYPE A.  
FT CHAIN 31 251  
FT DISULFID 117 128  
FT CONFLICT 6 6 K -> E (IN REF. 2).  
FT CONFLICT 17 18 VT -> MK (IN REF. 2).  
FT CONFLICT 25 35 SOEFAQDDPD -> LPKGICSTRPK (IN REF. 2).  
FT CONFLICT 40 40 H -> Q (IN REF. 2).  
FT CONFLICT 43 43 S -> N (IN REF. 2).  
FT CONFLICT 47 59 NLONTVELYEGDP -> TFKIVFPMRVTL (IN REF. 2).  
FT CONFLICT 129 129 I -> L (IN REF. 2).  
FT CONFLICT 165 178 TNKKMVTAAQELDYK -> QIKNGNCSRIYST (IN REF. 2).  
FT HELIX 36 38  
FT HELIX 42 44  
FT TURN 48 48  
FT HELIX 49 56  
FT STRAND 60 66  
FT STRAND 69 69  
FT TURN 73 74  
FT STRAND 75 78  
FT STRAND 82 82  
FT TURN 83 84  
FT STRAND 85 85  
FT STRAND 87 91  
FT HELIX 95 101  
FT TURN 102 103  
FT STRAND 105 110  
FT STRAND 113 113  
FT TURN 115 116  
FT STRAND 126 130  
FT STRAND 133 135  
FT TURN 137 138  
FT STRAND 140 153  
FT TURN 154 155  
FT STRAND 156 167  
FT STRAND 169 171  
FT HELIX 172 187  
FT STRAND 189 205

*Handwritten:* Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.

FT STRAND 212 215  
FT HELIX 224 227  
FT HELIX 228 231  
FT TURN 232 233  
FT STRAND 236 238  
FT TURN 239 241  
FT STRAND 243 249  
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCCBFC3 CRC64;  
Query Match 99.2%; Score 1169; DB 1; Length 251;  
Best Local Similarity 99.5%; Pred. No. 2.4e-82;  
Matches 220; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QQDDPSSQLHRSLSLVKNIQNTYFLYEGDPVTHENVKSDQLSHHLYNVSGPNYDKLKT 60  
Db 31 QQDDPSSQLHRSLSLVKNIQNTYFLYEGDPVTHENVKSDQLSHHLYNVSGPNYDKLKT 90  
QY 61 ELKQEMATLFDKKNVDYGVYVHLCYLCEAERSACIYGVVTHNHNHLEIPKKIVVK 120  
Db 91 ELKQEMATLFDKKNVDYGVYVHLCYLCEAERSACIYGVVTHNHNHLEIPKKIVVK 150  
QY 121 VSIDGIQSLSDIETNKKMVTAAQELDYKVRKYLTDNKLTYNGPSKYETGYIKFIPKKE 180  
Db 151 VSIDGIQSLSDIETNKKMVTAAQELDYKVRKYLTDNKLTYNGPSKYETGYIKFIPKKE 210  
QY 181 SFWDFPFPEPTQSKYIMLYKDNELDNTSQTIEVLTTK 221  
Db 211 SFWDFPFPEPTQSKYIMLYKDNELDNTSQTIEVLTTK 251  
RESULT 2  
FTXB STRAU STANDARD; PRT; 266 AA.  
ID -EXB STRAU  
AC P01552;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Enterotoxin type B precursor (SEB).  
ENB  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86168029; PubMed=3957869;  
RA Jones C.L., Khan S.A.;  
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus";  
RL J. Bacteriol. 166:29-33(1986).  
RN [2]  
RP SEQUENCE OF 40-91 FROM N.A.  
RX MEDLINE=85298255; PubMed=3898073;  
RA Raneli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;  
RT "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).  
RN [3]  
RP SEQUENCE OF 28-266 (S-6).  
RX MEDLINE=71007902; PubMed=5470821;  
RA Huang I.-Y., Bergdoll M.S.;  
RT "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence";  
RL J. Biol. Chem. 245:3518-3525(1970).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RX MEDLINE=93063291; PubMed=1436058;  
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;  
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen";  
RL Nature 359:801-806(1992).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MEC II.  
RX MEDLINE=94203282; PubMed=8152483;

RA Jardtzy T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,  
RA Chl Y.I., Stauffer C., Strominger J.L., Wiley D.C.;  
RT "Three-dimensional structure of a human class II histocompatibility  
RL molecule complexed with superantigen.";  
RN Nature 368:711-718(1994).  
[6]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.  
RX MEDLINE=99096298; PubMed=981971;  
RA Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,  
RA Karjalainen K., Mariuzza R.A.;  
RT "Three-dimensional structure of the complex between a T cell receptor  
RT beta chain and the superantigen staphylococcal enterotoxin B";  
RL Immunity 9:807-816(1998).  
[7]  
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
RX MEDLINE=98181012; PubMed=9514739;  
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;  
RT "Crystal structure of microbial superantigen staphylococcal  
RT enterotoxin B at 1.5-A resolution: implications for superantigen  
RT recognition by MHC class II molecules and T-cell receptors.";  
RL J. Mol. Biol. 277:61-79(1998).  
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication  
CC staphylococcal food poisoning syndrome. The illness characterized  
CC by high fever, hypotension, diarrhea, shock, and in some cases  
CC death.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin  
CC family.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
DR EMBL; M11118; AAA8550.1; -.  
DR PIR; S27360; ENSAB6.  
DR PDB; 1SEB; 20-JUN-96.  
DR PDB; 2SEB; 28-JAN-98.  
DR PDB; 3SEB; 27-MAY-98.  
DR PDB; 1SE3; 16-JUN-97.  
DR PDB; 1SE4; 15-OCT-97.  
DR PDB; 1SBB; 04-MAR-99.  
DR PDB; 1DSM; 14-MAR-01.  
DR PDB; 1DSX; 28-JUN-00.  
DR PDB; 1DSZ; 28-JUN-00.  
DR PDB; 1DGE; 28-JUN-00.  
DR InterPro; IPR00892; Bact endotox.  
DR InterPro; IPR006177; Bctrl tox.  
DR InterPro; IPR006123; Staph/Strep toxin.  
DR InterPro; IPR006173; Staph/Strep tox.  
DR Pfam; PF02876; Staph\_strep\_tox\_C; 1.  
DR Pfam; PF01123; Staph\_strep\_toxin; 1.  
DR PRINTS; PR00279; BACTELTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.  
FT SIGNAL 1 27  
FT CHAIN 28 266 ENTEROTOXIN TYPE B.  
FT DISULFID 120 140  
FT CONFLICT 56 58 DDN -> NND (IN REF. 3).  
FT CONFLICT 69 77 DQFLYFDLI -> NEFPDLYL (IN REF. 3).  
FT CONFLICT 118 118 MISSING (IN REF. 3).  
FT CONFLICT 128 130 DIN -> NID (IN REF. 3).  
FT CONFLICT 133 135 QTD -> ENT (IN REF. 3).  
FT CONFLICT 149 150 NG -> GN (IN REF. 3).  
FT CONFLICT 156 156 Y -> YV (IN REF. 3).  
FT CONFLICT 185 186 QE -> EQ (IN REF. 3).  
FT CONFLICT 233 233 D -> N (IN REF. 3).  
FT CONFLICT 246 247 DN -> ND (IN REF. 3).  
FT CONFLICT

FT STRAND 29 29  
FT HELIX 41 43  
FT STRAND 44 44  
FT TURN 48 48  
FT HELIX 49 52  
FT HELIX 53 55  
FT STRAND 60 66  
FT STRAND 69 69  
FT TURN 73 74  
FT STRAND 75 78  
FT TURN 83 85  
FT STRAND 90 94  
FT HELIX 98 104  
FT TURN 105 106  
FT STRAND 108 113  
FT STRAND 116 116  
FT TURN 118 119  
FT TURN 127 128  
FT STRAND 138 142  
FT STRAND 145 147  
FT TURN 149 150  
FT STRAND 152 165  
FT TURN 166 167  
FT STRAND 168 179  
FT STRAND 181 183  
FT HELIX 184 199  
FT STRAND 209 218  
FT TURN 219 220  
FT STRAND 221 226  
FT STRAND 232 232  
FT HELIX 237 241  
FT HELIX 242 246  
FT STRAND 249 251  
FT TURN 252 254  
FT STRAND 255 263  
SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;  
  
Query Match 48.6%; Score 572; DB 1; Length 266;  
Best Local Similarity 49.2%; Pred. No. 9e-37;  
Matches 116; Conservative 36; Mismatches 68; Indels 16; Gaps 5;  
  
QY 1 QQDPDPSSQLHRSLVKNL-QNIYFLYEGDPVTHENVKSVQDLSHLLIYNVSGP---NYD 56  
Db 30 QPDPKDELHKSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGND 89  
QY 57 KLKTELKNOEMATLFDKQKNDIYGVVEYHLCYLCENA-----ERSACIYGGVTNHE 107  
Db 90 NRVVEFKKDLADKYDKYDVFEGANYYYQCYFSKKTNDINSHQTKRCKTMYGGVTEHN 149  
QY 108 GNHLEIPKIKVWKSIDGICSLSPDIETNKKMVTAGELDYKVRKYLTDNKKQLYTNGESKY 167  
Db 150 GNQLDKYRSITRVFEDGKLLSFDVQTNKKVTAQELDYLTRHYLVKNKKLYEENNSPY 209  
QY 168 ETGYIKFIPKNKSWFDFPPEP--EPTQSKYLMYKNDTLDSTNSQIEVYLTK 221  
Db 210 ETGYIKFI-ENENSWFYDMMFADGKDFQSKYLMYNDKNQWVDSKDVKIEVYLTK 264  
  
RESULT 3  
ETC3\_STAM  
ID ETC3\_STAM STANDARD; PRT; 266 AA.  
AC P23313;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Enterotoxin type C-3 precursor (SEC3).  
GN ENVC3 OR SAV2009 OR SA1817.  
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),  
OS Staphylococcus aureus (strain N315), and  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=158878, 158879, 1380;  
RN [1]



DR PDB; 1140; 19-SEP-01.  
DR PDB; 1148; 19-SEP-01.  
DR PDB; 114X; 19-SEP-01.  
DR InterPro; IPR008992; Bact endotox.  
DR InterPro; IPR006177; Bactl tox.  
DR InterPro; IPR006123; Staph/Strep toxin.  
DR InterPro; IPR006126; Staph/Strep tox.  
DR InterPro; IPR006173; Staph tox OB.  
DR Pfam; PF02876; Staph\_strp\_tox\_C; 1.  
DR Pfam; PF01123; Staph\_strp\_tox; 1.  
DR PRINTS; PR00279; BACTRITOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;  
KW 3D-structure.  
FT SIGNAL 1 27 ENTEROTOXIN TYPE C-2.  
FT CHAIN 28 266  
FT DISULFID 120 137  
FT METAL 36 36 ZINC.  
FT METAL 110 110 ZINC.  
FT METAL 145 145 ZINC.  
FT METAL 149 149 ZINC.  
FT HELIX 35 37  
FT HELIX 41 43  
FT HELIX 44 44  
FT TURN 48 48  
FT HELIX 49 55  
FT STRAND 60 65  
FT STRAND 69 69  
FT TURN 73 74  
FT STRAND 75 79  
FT TURN 83 86  
FT STRAND 90 94  
FT HELIX 98 104  
FT TURN 105 106  
FT STRAND 109 113  
FT STRAND 116 116  
FT TURN 118 119  
FT TURN 128 129  
FT STRAND 136 139  
FT STRAND 142 144  
FT TURN 146 147  
FT STRAND 149 149  
FT HELIX 151 153  
FT STRAND 156 164  
FT TURN 165 166  
FT STRAND 167 176  
FT STRAND 178 178  
FT STRAND 180 182  
FT HELIX 183 198  
FT STRAND 208 216  
FT TURN 218 219  
FT STRAND 222 226  
FT STRAND 232 232  
FT HELIX 237 241  
FT HELIX 242 246  
FT STRAND 249 251  
FT STRAND 252 254  
FT TURN 255 263  
SQ SEQUENCE 266 AA; 8407FB18536FAC08 CRC64;  
Query Match 46.1%; Score 543; DB 1; Length 266;  
Best Local Similarity 46.4%; Pred. No. 1.5e-34;  
Matches 109; Conservative 45; Mismatches 67; Indels 14; Gaps 6;  
QY 1 QQQPDRPSQLRRSS-LVKNLQNIYFLYEGDPVTHENVKSVDDLSHLLIYVSG---PNYD 56  
DB 30 QPDPDPDLKSEFTGTGNGKYLDDHVSATKWSVDKFLAHLIYINISDKLKND 89  
QY 57 KLKTELKNQBMATLFDKNDYDIYGEYHLCYLQ--ENAEER----SACIYGVVTHHEGHN 110  
DB 90 KVATELLNEDLAKYKDEVDVDVYGSNYVNCYFSSKDNVGVKGTCTMYGGITKEGHN 149

QY 111 LEIP--KKIVVKVSDIGIQLSFDIFETNKQMTAQLDYKVRKYLTDNKQLYNGPSKYE 168  
DB 150 FDGNLQNLVIRVVENKRNITISFEVQTDKKSVAQELDIKARNFLINKNLVFNSSPYE 209  
QY 169 TGYIKFIPKPKESFWDFFPEP--EFTOSKYLMIYKDNFTLDSNTSQIEVYLTK 221  
DB 210 TGYIKFIENNGNTFWYDMPPAGDKFDQSKYLMYNDNKIVDSKSVKIEVHLTK 264  
RESULT 5  
ETC1 STAAU STANDARD; PRT; 266 AA.  
AC P01553;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Enterotoxin type C-1 precursor (SEC1).  
GN ETC1.  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88038352; PubMed=2823067;  
RA Bohach G.A., Schlievert P.M.;  
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to other pyrogenic toxins.";  
RL Mol. Gen. Genet. 209:15-20(1987).  
RN [2]  
RP SEQUENCE OF 28-266.  
RX MEDLINE=83213327; PubMed=6189824;  
RA Schmidt J.J., Spiero L.;  
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";  
RL J. Biol. Chem. 258:6300-6306(1983).  
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.  
CC  
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CC  
CC EMBL; X05815; CAA29260.1; -.  
DR PIR; S06356; ENSAC1.  
DR HSP; P34071; 1SE2.  
DR InterPro; IPR008992; Bact endotox.  
DR InterPro; IPR006177; Bactl tox.  
DR InterPro; IPR006123; Staph/Strep toxin.  
DR InterPro; IPR006126; Staph/Strep tox.  
DR InterPro; IPR006173; Staph tox OB.  
DR Pfam; PF02876; Staph\_strp\_tox\_C; 1.  
DR Pfam; PF01123; Staph\_strp\_tox; 1.  
DR PRINTS; PR00279; BACTRITOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Signal; Superantigen.  
FT SIGNAL 1 27  
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.  
FT DISULFID 120 137  
FT CONFLICT 177 177 D -> N (IN REF. 2).  
FT SEQUENCE 266 AA; 30546 MW; 3A7AB59A8986853B CRC64;  
SQ  
Query Match 46.0%; Score 542; DB 1; Length 266;  
Best Local Similarity 46.8%; Pred. No. 1.7e-34;  
Matches 110; Conservative 44; Mismatches 67; Indels 14; Gaps 6;

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QY 1 QODPDSQLHRSLSLVKNL-ONIFYLYEGDPVTHENVKSVLDQLSHHLYINVSQ---PNYD 56
DB 30 QDPDPFDELHKASKFTGLMKNKVLDDHYYSATKVKSVDFLAHLDIYINISDKKLKNDY 89
QY 57 KLKTELKNOEMATLFDKKNVDIYGVYHLYCLYC--ENAE- ----SACIYGGVTHNEGHN 110
DB 90 KVKTELLNEGLAKKYKDEVDVYGSNYVYCYFSKDNVGVKVTGCKTCMVGITKHGHN 149
QY 111 LEIP--KKIVVKVSDIGTQSLSDIETNKQVTAQELDYKVRKYLTDNKQLYTNGPSKYE 168
DB 150 PDNGNLQNLVLFVYENKENTISFEVQTDKSVTAQELDIKARNFLINKNLNLYEFPSSPYE 209
QY 169 TGYIKFIPKNKESFWDFPFP--BFTQSKYLMYKDNETLDSNTSQIEVLITK 221
DB 210 TGYIKFIENNGTFTYDMPAPGDXFDQSKYLMYNDNKTYDYSKVIEVHLITK 264

RESULT 6
ETXG-STAAU
ID ETXG STAAU STANDARD; PRT; 258 AA.
AC O85382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type G precursor (SEG).
GN ENTG OR SEG OR SAV1824 OR SA1642.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=158878, 158879, 1280;
RX [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP SEQUENCE FROM N.A.
RC STRAIN=MU50 / ATCC 700699, and N315;
RX MEDLINE=98298056; PubMed=9632603;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RL aureus".
RL Lancet 357:1225-1240(2001).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
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CC
CC ENBL; AF064773; AAC26660.1; -
CC ENBL; AP003363; BAB57986.1; -
CC ENBL; AP003135; BAB42910.1; -

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DR PIR; G89968; G89968.
DR HSP; P01552; ISBB.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superoxide; Complete proteome.
FT SIGNAL 1 25 ENTEROTOXIN TYPE G.
FT CHAIN 26 258 BY SIMILARITY.
FT DISULFID 116 133
SQ SEQUENCE 258 AA; 29940 MW; E2982101701D012C CRC64;

Query Match 39.7%; Score 468; DB 1; Length 258;
Best Local Similarity 43.8%; Pred. No. 7.4e-29;
Matches 102; Conservative 39; Mismatches 78; Indels 14; Gaps 4;

QY 1 QODPDSQLHRSLSLVKNL-ONIFYLYEGDPVTHENVKSVLDQLSHHLYINVSQPNYD 56
DB 26 QDPDPFDELHKASKFTGLMKNKVLDDHYYSATKVKSVDFLAHLDIYINISDKKLKNDY 85
QY 57 KLKTELKNOEMATLFDKKNVDIYGVYHLYCLYCENAE-----RSACIYGGVTHNEGHN 110
DB 86 EVKTELENTLANNYKDKKVDIFGVYFYTCIIPKSEPDINQNFQGCCMYGGLTFNSSEN 145
QY 111 LEIPKKIVVKVSDIGTQSLSDIETNKQVTAQELDYKVRKYLTDNKQLYTNGPSKYENG 170
DB 146 -ERDKLITVQVITDNRQSLGFTITTKNMVTTQELDYKARHMLTKKKLYEDFGSAFESG 204
QY 171 YIKFIPKNKESFWDFPFP--BFTQSKYLMYKDNETLDSNTSQIEVLIT 220
DB 205 YIKFTEKNNTSFWDFLPFKKELVFPVYKFLNYGDKVKVDSKIRKVEFLNT 257

RESULT 7
ETXD-STAAU
ID ETXD STAAU STANDARD; PRT; 258 AA.
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enterotoxin type D precursor (SED).
GN ENTG.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1280;
RX [1] SEQUENCE FROM N.A.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Iandolo J.J.,
RA "Genetic and molecular analyses of the gene encoding staphylococcal
RT enterotoxin D".
RL J. Bacteriol. 171:4799-4806(1989).
RN [2]
RN SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RP STRAIN=ATCC 23235;
RX MEDLINE=97157473; PubMed=9003758;
RA Sundstrom M., Abraham L., Antonsson P., Mehindate K., Mourad W.,
RA Dehlssten M.,
RA "The crystal structure of staphylococcal enterotoxin type D reveals
RT Zn2+-mediated homodimerization."
RL EMBO J. 15:6832-6840(1996).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- SUBUNIT: Homodimer; zinc-dependent.
CC -!- SUBCELLULAR LOCATION: Secreted.

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KW 3D-structure. 1 27  
FT SIGNAL 28  
FT CHAIN 211  
FT METAL 211  
FT METAL 249  
FT METAL 251  
FT METAL 251  
FT METAL 33  
FT METAL 39  
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FT METAL 257  
SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;  
Query Match 24.7%; Score 291.5; DB 1; Length 257;  
Best Local Similarity 35.1%; Pred. No. 2.2e-15;  
Matches 79; Conservative 42; Mismatches 85; Indels 19; Gaps 10;  
QY 7 SOLHSSLVNQLNFIYEGDPVTHENKVSVDQLSHLIYN---VSGPNYDKLTELK 63  
Db 40 SELQNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFGHPWYNDLLVGLG 96  
QY 64 NOEMATLFDKNDIYGVYVHLCVLCENASRACIYGVNHEGHELEIPKIVKVI 123  
Db 97 SKDANKYKGVDDIYGYIGYQC-AGTTPKTKCTGGVTLHDNNRLTEKKVPINLWI 155  
QY 124 DGIQ-SLSPD-IETKVMVTAQELDYKVRKYLTDNKLQYNGP--SKYETGYIKFIPK 179  
Db 156 DGKQTVTDIKVTKSKETVQELDLQARHVLHGKFLGYNLSDSPGKVGQGLIVFHSSE 215  
QY 180 ESFWDFEPPEFTOSKY---LMTYKDNETLDSNTQIEVYLT 220  
Db 216 STVSVDLFD---AGQYPTDILLRIYDNKTIENSENLHIDLYLT 256  
RESULT 10  
ETXH STAAW STANDARD; PRT; 241 AA.  
AC Q53585;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Enterotoxin type H precursor (SEH).  
GN ENTH OR SEH OR MW0051.  
OS Staphylococcus aureus (strain MW2), and  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=196620, 1280;  
RN [1]\_  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.  
RC STRAIN=D4508;  
RX MEDLINE=95053699; PubMed=7964453;  
RA Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,  
RA Fischetti V.A., Zabriskie J.B.;  
RT "Characterization and biological properties of a new staphylococcal  
RT exotoxin";  
RL J. Exp. Med. 180:1675-1683 (1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MW2;  
RX MEDLINE=22040717; PubMed=12044378;  
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,  
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,  
RA Yamamoto K., Hiramatsu K.;  
RT "Genome and virulence determinants of high virulence community-  
RT acquired MRSA";  
RL Lancet 359:1819-1827 (2002).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).  
RX MEDLINE=20444256; PubMed=10986116;  
RA Haekansson M., Petersson K., Nilsson H., Forsberg G., Bjoerk P.,  
RA Antonsson P., Svensson L.A.;  
RT "The crystal structure of staphylococcal enterotoxin H: implications  
RT for binding properties to MHC class II and TCR molecules.";  
RL J. Mol. Biol. 302:527-537 (2000).  
CC -!  
CC FUNCTION: Staphylococcal enterotoxins cause the intoxication  
CC staphylococcal food poisoning syndrome. The illness characterized  
CC by high fever, hypotension, diarrhea, shock, and in some cases  
CC death.  
CC -!  
CC COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary  
CC for the toxin interaction with MHC class II.  
CC -!  
CC SUBCELLULAR LOCATION: Secreted.  
CC -!  
CC SIMILARITY: Belongs to the staphylococcal/streptococcal toxin  
CC family.  
CC  
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CC  
CC EMBL; U11702; AAA19777.1; -.  
DR EMBL; AP004822; BAB93916.1; -.  
DR PDB; 1ENF; 10-JAN-01.  
DR PDB; 1EWC; 10-JAN-01.  
DR PDB; 1F77; 10-JAN-01.  
DR PDB; 1HX1; 27-JUN-01.  
DR InterPro; IPR008992; Bact\_endotox.  
DR InterPro; IPR006177; Bctrl\_tox.  
DR InterPro; IPR006123; Staph/Strep\_toxin.  
DR InterPro; IPR006173; Staph\_tox\_OB.  
DR Pfam; PF01123; Staph\_strep\_toxin; 1.  
DR Pfam; PF02876; Staph\_strep\_toxin; 1.  
DR PRINTS; PR00279; BACTSTREP\_TOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; FALSE\_NEG.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;  
KW 3D-structure; Complete proteome.  
FT SIGNAL 1 24  
FT CHAIN 25 241 ENTEROTOXIN TYPE H.  
FT METAL 230 230 ZINC.  
FT METAL 232 232 ZINC.  
FT DISULFID 106 116

SQ SEQUENCE 241 AA; 27858 MW; 70F77985877616CE CRC64;  
 Query Match 23.9%; Score 281.5; DB 1; Length 241;  
 Best Local Similarity 38.0%; Pred. No. 1.2e-14;  
 Matches 84; Conservative 33; Mismatches 87; Indels 17; Gaps 10;  
 QY 9 LHRSLVKN--LQNIYFLYEGDP--VTHENVK--SYDQLLSHLLIYVSGPNYDKLTKELKNQE 66  
 DB 27 LHKDSELTDLALANAYQY--NHPTIKENIKSDEISGEKDLIFRNQDGSNDLRYKFATAD 85  
 QY 67 MATLFDKQNDIYGVYHLC--YLCNAERSACIYGGV--TNEGHNLEIPKKIVVKVKSID 124  
 DB 86 LAQFKKNKNDIYGFASFYKKEKISNI--SECLYGGTLLNSE--KLAQSERVIGANVWD 141  
 QY 125 QIQLSFDIENKXNVTAQELDYKVRKYLTKNQKLYNGPSKYGTGVIKIPKKESEFW 184  
 DB 142 GIQKETELIRTKKNTVLQELDKIRKILSDKIYK--DSEISKGLIEFDMKTPRYSF 200  
 QY 185 DFFP---EPETQSKYLMYKDNFTLDS--NTSQIEVYLTK 221  
 DB 201 DIYDLKGENYDIDK---IYEDNKILKSDDISHDVNLTK 238  
 RESULT 11  
 SPEC\_STRPY STANDARD; PRT; 236 AA.  
 AC Q9X5C8  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Exotoxin type H precursor (SPE H).  
 GN SPEH OR SPY1008.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M15;  
 RX MEDLINE=99093428; PubMed=9874566;  
 RA Proft T, Moffatt S.L., Berkahn C.J., Fraser J.D.;  
 RT Identification and characterization of novel superantigens from  
 RT Streptococcus pyogenes.;  
 RL J. Exp. Med. 189:89-102 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;  
 RX MEDLINE=21192684; PubMed=11296296;  
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).  
 CC 1- FUNCTION: Mitogenic for human peripheral blood lymphocytes.  
 CC 1- SUBUNIT: Binds to major histocompatibility complex class II beta  
 CC chain.  
 CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin  
 CC family.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF124500; AAD30989.1; -;  
 CC EMBL; A8006546; AAK33907.1; -;  
 CC FDB; 1ET9; 24-MAY-00.  
 CC FDB; 1EU4; 24-MAY-00.

DR InterPro; IPR008992; Bact\_endotox.  
 DR InterPro; IPR006123; Staph/Strep\_toxin.  
 DR InterPro; IPR006126; Staph/Strep\_tox.  
 DR InterPro; IPR006173; Staph\_tox OB.  
 DR Pfam; PF02876; Staph\_Strep\_tox C; 1.  
 DR Pfam; PF01123; Staph\_Strep\_toxin; 1.  
 DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; FALSE\_NEG.  
 DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 KW Toxin; Signal; Complete proteome; 3D-structure.  
 FT SIGNAL 1 32 POTENTIAL.  
 FT CHAIN 33 236 EXOTOXIN TYPE H.  
 SQ SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;  
 Query Match 17.8%; Score 209.5; DB 1; Length 236;  
 Best Local Similarity 31.4%; Pred. No. 3.5e-09;  
 Matches 66; Conservative 32; Mismatches 93; Indels 19; Gaps 9;  
 QY 17 NLQNIYFLYEGDP--VTHENVK--SYDQLLSHLLIYVSGPNYDKLTKELKNQMATLFRD 73  
 DB 39 NRHNLESYKHDNSLIEADSIKNSPDIVTSHMLKYSVKDKN---LSVPFEKDWISQEFKD 95  
 QY 74 KNVDIYGVYHLCYLCNAERSACIYGGV--TNEGHNLEIPKKIVVKVKSIDGICLSLF 131  
 DB 96 KEVDIYALSQAEVCE--CPGKRYEA--FGGITITNSEKEIKVP---VNVWKSQOQPM 148  
 QY 132 DIETNKKMVTAEOLDYKVRKYLTKNQKLYNGPSKYGTGVIKIPKKESEFWF--FFPE 189  
 DB 149 FITVNPVKVTAQEVDIKVRKLLIKKYDIYNNREQYKSGVTDLNSGKDIVEDLYYFGN 208  
 QY 190 PEFTQSKYLMYKDNFTLDSNTSQIEVYLTK 219  
 DB 209 GDF--NSMLKIYSNNRIDSTQFHDVVIS 236  
 RESULT 12  
 SPEC\_STRPY STANDARD; PRT; 235 AA.  
 AC P13380;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Exotoxin type C precursor (SPE C).  
 GN SPEC OR SPY0711.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.  
 RC STRAIN=TI8P / MGAS 1585;  
 RX MEDLINE=88314303; PubMed=3045005;  
 RA Goshorn S.C., Schlievert P.M.;  
 RA "Nucleotide sequence of streptococcal pyrogenic exotoxin type C.";  
 RL Infect. Immun. 56:2518-2520 (1988).  
 RN [2]  
 RP REVISIONS TO 21-26.  
 RC STRAIN=TI8P / MGAS 1585;  
 RX MEDLINE=92363541; PubMed=1500157;  
 RA Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;  
 RT "Molecular population genetic evidence of horizontal spread of two  
 RT alleles of the pyrogenic exotoxin C gene (speC) among pathogenic  
 RT clones of Streptococcus pyogenes.";  
 RL Infect. Immun. 60:3513-3517 (1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;  
 RX MEDLINE=21192684; PubMed=11296296;  
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
 RT "Complete genome sequence of an M1 strain of Streptococcus  
 RT pyogenes.";

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Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
[4]
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
RX MEDLINE=97397352; PubMed=9253413;
RA Rousset A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
RT "Crystal structure of the streptococcal superantigen SPE-C:
RT dimerization and zinc binding suggest a novel mode of interaction
RT with MHC class II molecules."
RL Nat. Struct. Biol. 4:1635-643 (1997).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic
CC fever.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: M35514; AA27017.1; ALT_SEQ.
CC EMBL: M97156; AAB59091.1; -.
CC EMBL: M97157; AAB59092.1; -.
CC EMBL: AE006523; AA333664.1; -.
CC PIR: A30509; A30509.
CC PIR: A44799; A44799.
CC PDB: 1ANS; 29-APR-98.
CC PDB: 1KTK; 07-JUN-02.
CC InterPro: IPR008992; Bact_endotox.
CC InterPro: IPR006177; Bcstrl_tox.
CC InterPro: IPR006123; Staph/Strep_toxin.
CC InterPro: IPR006126; Staph/Strep_tox.
CC InterPro: IPR006173; Staph_tox_OB.
CC Pfam: PF02876; Staph_strp_tox_C; 1.
CC Pfam: PF01123; Staph_strp_toxin; 1.
CC PRINTS: PR00279; BACTERIOTOXIN.
CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
CC Toxin; Signal; 3D-structure; Complete proteome.
CC
CC SIGNAL 1 27 EXOTOXIN TYPE C.
CC CHAIN 28 235 N -> D (IN REF. 1).
CC CONFLICT 53 53
CC HELIX 33 44
CC STRAND 49 59
CC STRAND 63 67
CC HELIX 69 72
CC TURN 74 75
CC STRAND 77 81
CC HELIX 84 87
CC TURN 88 89
CC TURN 92 93
CC STRAND 95 100
CC TURN 108 109
CC STRAND 110 114
CC STRAND 117 119
CC STRAND 127 128
CC STRAND 131 135
CC TURN 136 137
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CC STRAND 153 155
CC HELIX 156 171
CC TURN 173 174
CC TURN 176 177
CC STRAND 182 189
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FT TURN 190 191
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FT STRAND 226 235
SQ SEQUENCE 235 AA; 27371 MW; 070534ABB952C1E0 CRC64;

Query Match 17.4%; Score 205; DB 1; Length 235;
Best Local Similarity 29.5%; Pred. No. 7.7e-09;
Matches 67; Conservative 47; Mismatches 83; Indels 30; Gaps 12;

Qy 7 SQLHRSLSVKNLONI-----YFLYEGDPVTHENVKSVQDQLLSHLIYNVSPNYD----KL 58
Db 22 SPIKSDSKDISNVKSDLLIAYITIPDYKNCR-VNFSTHTL--NIDTKRGKDYI 78
Qy 59 ELKLNEMATLFDKKNVDIYGYEYHLCYLCEAERSACIYGVVT---NHEGNHLEIPK 115
Db 79 SSEMSEASQKFKRHHVDVEGL-FYIL-----NSHTGEIYGGITPAQNNKVNH----- 127
Qy 116 KIVKVISIDG--TQSLSFDIETKKNVTAQELDYKRYKLYTDNKQLYTNGSPSKYGVYIK 173
Db 128 KLLGNLFISGESQCNLNKKIILEKDIVTFOEIDFKIRKYLMDNYKIY-DATSPFVSGRIE 186
Qy 174 FIPKNKESFDFPPEP-EFTQSKYLMYKDNETLD-SNTSQIEVYL 218
Db 187 IGYKDGKHEQIDLFDSNEGTRSDIFAKYKDNRIINKNKFSHFDIYL 233

RESULT 13
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ID _SPEG STRPY STANDARD; PRT; 234 AA.
AC Q9X5C7;
DC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Exotoxin type G precursor (SPE G).
GN SPEG OR SPY0212.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OC Streptococcus
OX NCBI_TaxID=1314;
RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1;
RX MEDLINE=99093428; PubMed=9874566;
RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RL Streptococcus pyogenes."
RN J. Exp. Med. 189:89-102 (1999).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., McLaughlin R.;
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
CC -!- FUNCTION: Mitogenic for human peripheral blood lymphocytes.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
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EMBL; AF124499; AAD30988.1; -  
EMBL; AE006489; AAK33303.1; -  
HSP; P13380; IAN8.  
InterPro; IPR008992; Bact\_endotox.  
InterPro; IPR006177; Bct\_1 tox.  
InterPro; IPR006123; Staph/Strep\_toxin.  
InterPro; IPR006126; Staph/Strep\_tox.  
InterPro; IPR006173; Staph\_tox OB.  
Pfam; PF02876; Staph\_Strep\_tox C; 1.  
Pfam; PF01123; Staph\_Strep\_toxin; 1.  
PRINTS; PR00279; BACTRLTOXIN.  
PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; FALSE\_NEG.  
PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
Toxin; Signal; Complete proteome.  
FT CHAIN 1 24 POTENTIAL.  
FT SIGNAL 25 234 EXOTOXIN TYPE G.  
SQ SEQUENCE 234 AA; 27262 MW; 49525C49E4BA2052 CRC64;

Query Match 13.8%; Score 162; DB 1; Length 234;  
Best Local Similarity 24.1%; Pred. No. 1.5e-05;  
Matches 53; Conservative 42; Mismatches 81; Indels 44; Gaps 10;

QY 33 ENKVSVDQLSHLLINVSQPNYDK-----LKTENKQEMA----- 68  
Db 26 ENLKDKRSL--RFAYNIHPCDYENVEIAFVNTNSIHINTKORSECLYVDSIVSLGIT 83  
QY 69 -TLFDKNDVIVVEYHYLCYLCENARACIYGGVTHN--EGNHLEIPKIVKVSIDG 125  
Db 84 DQFIKGVDFVGLPYNFPPYVDN-----IYGVKHSNGNK---SLQFVGLNQDG 134  
QY 126 IQSL--SFDIETNKQMTVAQELDYKVKYLTNQLYNGPSKYTGVIKIPKNSBFW 183  
Db 135 KETLSEAVRIKKQFTLQDFDKIRKFMKYNII--DSEGYTSGSLFLATKDSKHYE 193  
QY 184 DFFPPEPE--FTQSKYLMYKNETLDS--NTSQIEVILT 220  
Db 194 VDLFNKDKLSRDSFFKAYKONKIFNSEISHFDIYLT 233

RESULT 14  
TSST\_STAAU STANDARD; PRT; 234 AA.  
AC P06886;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Toxic shock syndrome toxin-1 precursor (TSST-1).  
GN TST.  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=87057222; PubMed=3782090;  
RA Blomster-Hautamaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,  
RA Schlievert P.M.;  
RT "The nucleotide and partial amino acid sequence of toxic shock  
RL syndrome toxin-1.";  
RL J. Biol. Chem. 261:15783-15786(1986).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RX MEDLINE=94150598; PubMed=8107781;  
RA Acharya K.R., Passalacqua E.F., Jones E.Y., Harlos K., Stuart D.I.,  
RA Rehms R.D., Tranter H.S.;  
RT "Structural basis of superantigen action inferred from crystal  
RL structure of toxic-shock syndrome toxin-1.";  
RL Nature 367:94-97(1994).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RX MEDLINE=94092653; PubMed=8268150;

Prasad G.S., Earhart C.A., Murray D.L., Novick R.P., Schlievert P.M.,  
Ohlendorf D.H.;  
RT "Structure of toxic shock syndrome toxin 1.";  
RL Biochemistry 32:13761-13766(1993).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS).  
RX MEDLINE=96319751; PubMed=8759320;  
RA Pappasgiorgiou A.C., Brehm R.D., Leonidas D.D., Tranter H.S.,  
RA Acharya K.R.;  
RT "The refined crystal structure of toxic shock syndrome toxin-1 at  
RT 2.07-A resolution.";  
RL J. Mol. Biol. 260:553-569(1996).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).  
RX MEDLINE=97337442; PubMed=9194182;  
RA Praesad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,  
RA Dinges M.M., Cook W.J., Schlievert P.M., Ohlendorf D.H.;  
RT "Refined structures of three crystal forms of toxic shock syndrome  
RT toxin-1 and of a tetramutant with reduced activity.";  
RL Protein Sci. 6:1220-1227(1997).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.  
RX MEDLINE=98254504; PubMed=9585531;  
RA Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,  
RA Schlievert P.M., Ohlendorf D.H.;  
RT "Structures of five mutants of toxic shock syndrome toxin-1 with  
RT reduced biological activity.";  
RL Biochemistry 37:7194-7202(1998).  
CC -|- FUNCTION: Responsible for the symptoms of toxic shock syndrome.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin  
CC family.  
CC  
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EMBL; J02615; AAA26682.1; -  
PIR; A24606; XCSA91.  
DR PDB; 2TSS; 24-DEC-97.  
DR PDB; 3TSS; 24-DEC-97.  
DR PDB; 4TSS; 24-DEC-97.  
DR PDB; 5TSS; 24-DEC-97.  
DR PDB; 1Q1L; 12-AUG-97.  
DR PDB; 2Q1L; 12-AUG-97.  
DR PDB; 1AW7; 18-NOV-98.  
DR PDB; 1T82; 16-DEC-98.  
DR PDB; 1T83; 16-DEC-98.  
DR PDB; 1T84; 16-DEC-98.  
DR PDB; 1T85; 16-DEC-98.  
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DR InterPro; IPR006123; Staph/Strep\_toxin.  
DR InterPro; IPR006126; Staph/Strep\_tox.  
DR InterPro; IPR008375; Staph\_exotoxin.  
DR InterPro; IPR006173; Staph\_tox OB.  
DR InterPro; IPR006125; Staph\_toxin.  
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DR Pfam; PF01123; Staph\_Strep\_toxin; 1.  
DR PRINTS; PR01800; STAPHSTOXIN.  
DR PRINTS; PR01501; TOXICSSTOXIN.  
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DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Toxin; Superantigen; Signal; 3D-structure.  
FT SIGNAL 1 40  
FT CHAIN 41 234 TOXIC SHOCK SYNDROME TOXIN-1.  
FT HELIX 46 54  
FT STRAND 58 69  
FT TURN 70 71  
FT STRAND 72 76

FT TURN 78 79  
FT STRAND 82 86  
FT TURN 90 91  
FT TURN 98 99  
FT STRAND 101 108  
FT STRAND 113 114  
FT TURN 116 117  
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FT STRAND 128 129  
FT STRAND 133 138  
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FT STRAND 149 151  
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FT STRAND 163 164  
FT STRAND 166 181  
FT TURN 183 185  
FT TURN 187 188  
FT STRAND 192 198  
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FT STRAND 203 207  
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FT TURN 214 216  
FT STRAND 221 222  
FT HELIX 223 225  
FT STRAND 226 234  
SQ SEQUENCE 234 AA; 26306 MW; E95789FF9A1D7AB4 CRC64;  
  
Query Match 8.6%; Score 101; DB 1; Length 234;  
Best Local Similarity 22.6%; Pred. No. 0.65;  
Matches 48; Conservative 31; Mismatches 99; Indels 34; Gaps 6;  
  
QY 3 DDPQLHSSLVK-----NLQNIYFLYEGDPVTHENVKSVDPQLSHLLIYVNSG-- 52  
DB 23 DTFVPLSGNQIIKTAKASTNDNIKDLWDYSSGSDTFTNSVLNDSLGSWRKIKTDGSI 82  
  
QY 53 -----PNYDKLTAKNQEMATLFDKKNVDIYGVYHYHLCYLCENASACIYGGVTN 105  
DB 83 SLIIIPSPYSPAFIKGKGVLDNTRKTKSQHTSGTVIHF-----QISGVTN 130  
  
QY 106 HGNHLEIPKKIVKVSINDIGQS-LSFDIETNKKWTAQELDYKYKYLTDNKKQLYTNGP 164  
DB 131 TE--KLPTIEFLPKVYKHGKDSPLKYGPKFKKQLAISTLDFEIRHQITQIHGJYRS-- 186  
  
QY 165 SKYETGYIKFIPKNKESFWDFPFPEFTQSK 196  
DB 187 SKTGGYWKITWNDGSGTYQSDLSKKEFYNTK 218  
  
RESULT 15  
DSCI HUMAN STANDARD; PRT; 894 AA.  
AC Q08554; HUMAN  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Desmocollin 1A/1B precursor (Desmosomal glycoprotein 2/3) (DG2/DG3).  
GN DSCI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Foreskin;  
RA MEDLINE=93283249; PubMed=8507556;  
RA Theis D.G., Koch P.J., Franke W.W.;  
RT "Differential synthesis of type 1 and type 2 desmocollin mRNAs in  
RT human stratified epithelia.";  
RL Int. J. Dev. Biol. 37:101-110(1993).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Foreskin;

RA Zimbelmann R.;  
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=94116981; PubMed=8288219;  
RA King I.A., Arneemann J., Spurr N.K., Buxton R.S.;  
RT "Cloning of the cDNA (DSCI) coding for human type 1 desmocollin and  
RT its assignment to chromosome 18";  
RL Genomics 18:185-194(1993).  
RN [4]  
RP SEQUENCE OF 135-151 AND 283-292.  
RX MEDLINE=91323543; PubMed=1713860;  
RA King I.A., Magee A.I., Rees D.A., Buxton R.S.;  
RT "Keratinization is associated with the expression of a new protein  
RT related to the desmosomal cadherins DGI/III";  
RL FEBS Lett. 286:9-12(1991).  
CC -!- FUNCTION: Component of intercellular desmosome junctions. Involved  
CC in the interaction of plaque proteins and intermediate filaments  
CC mediating cell-cell adhesion. May contribute to epidermal cell  
CC positioning (stratification) by mediating differential  
CC adhesiveness between cells that express different isoforms. Linked  
CC to the keratinization of epithelial tissues.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1A; Synonyms=DG2;  
CC IsoId=Q08554-1; Sequence=Displayed;  
CC Name=1B; Synonyms=DG3;  
CC IsoId=Q08554-2; Sequence=VSP\_000651, VSP\_000652;  
CC -!- TISSUE SPECIFICITY: Strongly expressed in epidermis, less in lymph  
CC node and tongue.  
CC -!- DOMAIN: Calcium may be bound by the cadherin-like repeats  
CC (Potential).  
CC -!- SIMILARITY: Contains 5 cadherin domains.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC  
DB EMBL; Z34522; CAA84279.1; -;  
DB EMBL; Z34522; CAA84278.1; -;  
DB EMBL; X72925; CAA51428.1; -;  
DB EMBL; X72925; CAA51429.1; -;  
DB PIR; I37281; I37281.  
DB PIR; I37282; I37282.  
DB HSSP; P15116; INCJ.  
DB Genew; HGNC:3035; DSCI.  
DB MIM; 125643; -;  
DB GO; GO:0005921; C:gap junction; TAS.  
DB GO; GO:0005624; C:membrane fraction; TAS.  
DB InterPro; IPR002126; Cadherin.  
DB Pfam; PF00028; cadherin; 5.  
DB PRINTS; PR00205; CADHERIN.  
DB SMART; SM00112; CA; 5.  
DB PROSITE; PS00232; CADHERIN 1; 3.  
DB PROSITE; PS00268; CADHERIN 2; 5.  
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;  
KW Cytoskeleton; Calcium-binding; Alternative splicing.  
FT SIGNAL 1 29  
FT PROPEP 30 134  
FT CHAIN 135 894  
FT DOMAIN 135 691  
FT TRANSMEM 692 714  
FT DOMAIN 715 894  
FT DOMAIN 135 242  
FT DOMAIN 243 354  
FT DOMAIN 355 471  
FT DOMAIN 472 575  
FT DOMAIN

FT	DOMAIN	576	682	CADHERIN 5.
FT	CARBOHYD	165	165	N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD	546	546	N-LINKED (GLCNAC... ) (POTENTIAL).
FT	VARSPPLIC	830	840	KVYLCGGDEEH -> ESIRGHTLIKN (in isoform 1B).
FT	VARSPPLIC	841	894	/FTid=VSP_000651.
FT	VARSPPLIC	132	132	Missing (in isoform 1B).
FT	CONFLICT	132	132	/FTid=VSP_000652.
FT	CONFLICT	132	132	T -> S (IN REF. 3).
SQ	SEQUENCE	894 AA;	100044 MW;	44BA33038699E3E1 CRC64;

Query Match 8.6%; Score 101; DB 1; Length 894;  
Best Local Similarity 19.8%; Pred. No. 3.2;  
Matches 51; Conservative 43; Mismatches 79; Indels 84; Gaps 10;

Qy	4	PDPQLHRSLLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHLLIYNVSGPNYDKLXTELK	63
Db	138	PIPASLMENSLGPPFQHV-----QQIQS-DAAQNTIFYSISGGVGRPEPNLF	185
Qy	64	NOEMAT--LPKDKNDIVGVYHLYCLCENAEASACIYGVGNHGNHLEIPKKIVVKV	121
Db	186	YIEKDTGDFCTRSIDREKYEQF-----ALYGVATTADGYAPEYPLPLIKI	232
Qy	122	SIDGIQSLSFIE-----TNKQNVTAQELD-----YKVKYLTDNKQ	158
Db	233	EDNDNAPYFEHRTFTVPENCERSGTSVGKVTATDLDEPDTLHRLKYLKIQIIPDHPX	292
Qy	159	LYTNGPSKYETGYI----KFIPKNKESFW-----PDFF-----	187
Db	293	HFSIHP---DTGVITTTTTPFDREKCDTYQLIMEVRDMGGQPFGLFNTGTITISLEDND	349
Qy	188	PEPEFTQSKYLMYKDN	204
Db	350	NPPSFTSTSYTVEEEN	366

Search completed: May 7, 2004, 12:08:08  
Job time : 19 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 12:04:53 ; Search time 46 Seconds  
(without alignments)  
1515.859 Million cell updates/sec

Title: US-10-625-221-14  
Perfect score: 1178  
Sequence: 1 QDDPPSQLHRSLLVKNLQN.....KDNETLDSNTSQIEVLYTTK 221

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1168	99.2	251	16 Q8K6K5	Q8K6K5 streptococc
2	1134	96.3	236	2 P97163	P97163 streptococc
3	1133	96.2	236	2 Q54779	Q54779 streptococc
4	1128	95.8	236	2 Q57453	Q57453 streptococc
5	1125	95.5	222	2 Q9R331	Q9R331 streptococc
6	1025	87.0	236	2 Q54596	Q54596 streptococc
7	1011	85.8	222	2 Q9S524	Q9S524 streptococc
8	1011	85.8	222	2 Q938P4	Q938P4 streptococc
9	549	46.6	239	2 Q53678	Q53678 streptococc
10	549	46.5	271	2 Q9F0L6	Q9F0L6 streptococc
11	548	46.5	239	2 Q06532	Q06532 streptococc
12	547	46.4	239	2 Q06533	Q06533 streptococc
13	547	46.4	266	16 Q8NXJ6	Q8NXJ6 streptococc
14	546	46.3	239	2 Q05157	Q05157 streptococc
15	546	46.3	239	2 Q06531	Q06531 streptococc
16	542	46.0	239	2 Q06535	Q06535 streptococc

#### ALIGNMENTS

#### RESULT 1

Q8K6K5 Q8K6K5 PRELIMINARY; PRT; 251 AA.  
ID Q8K6K5  
AC Q8K6K5  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Exotoxin type A, phage associated (SpeA precursor).  
GN SPEA3 OR SPYM3\_1301 OR SP80560.  
OS Streptococcus pyogenes (serotype M3).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=198466;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MGAS315 / Serotype M3;  
RX MEDLINE=22133808; PubMed=1212206;  
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,  
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S., Parkins L.D.,  
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.  
RA Schlievert P.M., Musser J.M.;  
RA "Genome sequence of a serotype M3 strain of Group A Streptococcus;  
RT phage-encoded toxins, the high-virulence phenotype, and clone  
RT emergence";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SSI-1 / Serotype M3;  
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,  
Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,  
Hayashi H., Hamada S.;  
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis  
of S. pyogenes SSI-1, SP370 and MGAS8232";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF014161; AAC79908.1;  
DR EMBL; AF005142; AAC63655.1;  
DR FIR; A60108; A60108.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0015070; F:toxin activity; IEA.

Q9R5X4 staphylococ  
Q06534 staphylococ  
Q54771 streptococ  
Q54738 streptococ  
Q54739 streptococ  
Q936G4 staphylococ  
Q8R177 staphylococ  
Q9EM3 staphylococ  
Q9ZNF2 staphylococ  
Q99T49 staphylococ  
Q99T46 staphylococ  
Q9EM8 staphylococ  
Q9EM3 staphylococ  
Q9EM3 staphylococ  
Q93IM4 staphylococ  
Q85217 staphylococ  
Q9EM5 staphylococ  
Q9F0L7 staphylococ  
Q8NXJ5 staphylococ  
Q8R176 staphylococ  
Q53585 staphylococ  
Q99T47 staphylococ  
Q9EM7 staphylococ  
Q8V1W7 staphylococ  
Q8NW97 staphylococ  
Q93CC6 staphylococ  
Q8NM3 staphylococ  
Q8NM2 staphylococ  
Q54476 staphylococ

537 45.6 234 2 Q9R5X4  
537 45.6 239 2 Q06534  
517.5 43.9 260 2 Q54771  
512.5 43.5 260 2 Q54738  
512.5 43.5 260 16 Q54739  
509 43.2 259 2 Q936G4  
468 39.7 233 2 Q8R177  
458 38.9 238 2 Q9EM3  
455 38.6 238 2 Q9ZNF2  
337 28.6 136 16 Q99T49  
323.5 27.5 261 2 Q99T46  
323.5 27.5 261 2 Q9EM8  
315.5 26.8 260 16 Q99SU3  
297.5 25.3 258 16 Q9EM3  
293.5 24.9 260 16 Q93IM4  
291.5 24.7 268 2 Q85217  
285.5 24.2 108 2 Q9EM5  
284 24.1 240 16 Q9F0L7  
283 24.0 240 16 Q8NXJ5  
281.5 23.9 217 2 Q8R176  
281.5 23.9 241 16 Q53585  
285.5 22.5 239 16 Q99T47  
264.5 22.5 239 2 Q9EM7  
246.5 20.9 256 2 Q8V1W7  
246 20.9 229 16 Q8NW97  
245.5 20.8 242 2 Q93CC6  
243.5 20.7 242 16 Q8NM3  
237 20.1 242 16 Q8NM2  
235 19.9 242 2 Q54476

```
GO; GO:0009405; P: pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Pfam; PF02876; Staph_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
DR SEQUENCE 251 AA; 29260 MW; 05E782CD8A01BFCD5 CRC64;

Query Match 99.2%; Score 1168; DB 16; Length 251;
Best Local Similarity 99.1%; Pred. No. 5e-78;
Matches 219; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QODPPPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSDQLSHHLYNVSGPNYDKLKT 60
DB 31 QODPPPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSDQLSHHLYNVSGPNYDKLKT 90
QY 61 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTHNHEGNHLEIPKKIYVK 120
DB 91 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTHNHEGNHLEIPKKIYVK 150
QY 121 VSDIGIQLSFDIETNKQVTAQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKKE 180
DB 151 VSDIGIQLSFDIETNKQVTAQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKKE 210
QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQIEVLYITK 221
DB 211 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQIEVLYITK 251

RESULT 2
P97163 PRELIMINARY; PRT; 236 AA.
AC P97163; P97164;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Type A exotoxin precursor (fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156, and MGAS500;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61556; CAA43754.1; -
DR EMBL; X61557; CAA43755.1; -
DR EMBL; X61560; CAA43758.1; -
DR EMBL; X61555; CAA43753.1; -
DR EMBL; X61558; CAA43756.1; -
DR EMBL; X61559; CAA43757.1; -
DR EMBL; X61554; CAA43752.1; -
DR PIR; A60108; A60108.
DR HSSP; P08095; 1B1Z.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P: pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR InterPro; IPR006126; Staph/Strep_tox.

GO; GO:0009405; P: pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
DR SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 96.3%; Score 1134; DB 2; Length 236;
Best Local Similarity 99.5%; Pred. No. 1.5e-75;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QODPPPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSDQLSHHLYNVSGPNYDKLKT 60
DB 23 QODPPPSQLHRSSLVKLNQNIYFLYEGDPVTHENVKSDQLSHHLYNVSGPNYDKLKT 82
QY 61 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTHNHEGNHLEIPKKIYVK 120
DB 83 ELKQEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTHNHEGNHLEIPKKIYVK 142
QY 121 VSDIGIQLSFDIETNKQVTAQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKKE 180
DB 143 VSDIGIQLSFDIETNKQVTAQELDYKVRKYLTNDKQLYTNGPSKYETGYIKFIPKKE 202
QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQI 214
DB 203 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQI 236

RESULT 3
Q54779 PRELIMINARY; PRT; 236 AA.
AC Q54779; Q54736; Q54740; Q54741;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Type A exotoxin precursor (fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, and MGAS495;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61569; CAA43767.1; -
DR EMBL; X61572; CAA43770.1; -
DR EMBL; X61568; CAA43766.1; -
DR EMBL; X61570; CAA43768.1; -
DR EMBL; X61571; CAA43769.1; -
DR PIR; A60108; A60108.
DR HSSP; P08095; 1B1Z.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P: pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR InterPro; IPR006126; Staph/Strep_tox.
```



180 PIPNKE  
 180 PIPNKE  
 202 PIPNKE  
 202 PIPNKE

Best Local Similarity 99.5%; Pred. No. 6.2e-75;  
Matches 211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQDPDPSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHSHLIYVSGPNYDKLKT 60  
DB 11 QQDPDPSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHSHLIYVSGPNYDKLKT 70

QY 61 ELKNOEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120  
DB 71 ELKNOEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 130

QY 121 VSIDGIQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKKE 180  
DB 131 VSIDGIQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKKE 190

QY 181 SFWDFPPEPFTQSKYLMYKONETLDSNTS 212  
DB 191 SFWDFPPEPFTQSKYLMYKONETLDSNTS 222

RESULT 6

Q54696 PRELIMINARY; PRT; 236 AA.  
AC Q54696;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Type A exotoxin precursor (Fragment).  
GN SPEA.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MGAS156;  
RX MEDLINE=92044323; PubMed=1940804;  
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;  
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes";  
RL J. Exp. Med. 174:1271-1274 (1991).  
DR EMBL; X61573; CAA43771.1; -;  
DR PIR; S18789; S18789.  
DR HSSP; P08095; 1B1Z.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0015070; F:toxin activity; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR008992; Bact\_endotox.  
DR InterPro; IPR006177; Bctrl\_tox.  
DR InterPro; IPR006123; Staph/Strep\_toxin.  
DR InterPro; IPR006173; Staph/Strep\_tox.  
DR Pfam; PF01123; Staph\_strep\_toxin\_1.  
DR Pfam; PF02876; Staph\_strep\_toxin\_C; 1.  
DR PRINTS; PR00279; BACTRLTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
KW Signal.  
FT NON\_TER 1  
FT SIGNAL <1 22 POTENTIAL.  
FT CHAIN 23 >236 TYPE A EXOTOXIN.  
FT NON\_TER 236  
SQ SEQUENCE 236 AA; 27575 MW; 70F54120B79127DF CRC64;

Query Match 89.0%; Score 1025; DB 2; Length 236;  
Best Local Similarity 89.7%; Pred. No. 1.4e-67;  
Matches 192; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 QQDPDPSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHSHLIYVSGPNYDKLKT 60  
DB 23 QQDPDPSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHSHLIYVSGPNYDKLKT 82

QY 61 ELKNOEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120  
DB 83 ELKNOEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 142

QY 121 VSIDGIQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKKE 180  
DB 143 VSIDGIQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKKE 202

QY 181 SFWDFPPEPFTQSKYLMYKONETLDSNTS 214  
DB 203 TFWDFPPEPFTQSKYLMYKONETLDSNTS 236

RESULT 7

Q5524 PRELIMINARY; PRT; 222 AA.  
AC Q5524;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Exotoxin type A (Fragment).  
GN SPEA.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DN633;  
RX MEDLINE=99137798; PubMed=9952369;  
RA Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,  
RA Hollingshead S.K., Beall B.;  
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci";  
RL J. Infect. Dis. 179:627-636 (1999).  
DR EMBL; AF029051; AAD21315.1; -;  
DR HSSP; P08095; 1B1Z.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0015070; F:toxin activity; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR008992; Bact\_endotox.  
DR InterPro; IPR006177; Bctrl\_tox.  
DR InterPro; IPR006123; Staph/Strep\_toxin.  
DR InterPro; IPR006173; Staph/Strep\_tox.  
DR Pfam; PF01123; Staph\_strep\_toxin\_1.  
DR Pfam; PF02876; Staph\_strep\_toxin\_C; 1.  
DR PRINTS; PR00279; BACTRLTOXIN.  
DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
FT NON\_TER 1  
FT NON\_TER 222  
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 85.8%; Score 1011; DB 2; Length 222;  
Best Local Similarity 89.2%; Pred. No. 1.4e-66;  
Matches 189; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 QQDPDPSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHSHLIYVSGPNYDKLKT 60  
DB 11 QQDPDPSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHSHLIYVSGPNYDKLKT 70

QY 61 ELKNOEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 120  
DB 71 ELKNOEMATLFDKKNVDIYGVYHYHLCYLCEAERSACIYGGVTNHEGHNHLEIPKKIVVK 130

QY 121 VSIDGIQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKKE 180  
DB 131 VSIDGIQSLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYETGYIKFIPKKE 190

QY 181 SFWDFPPEPFTQSKYLMYKONETLDSNTS 212  
DB 191 TFWDFPPEPFTQSKYLMYKONETLDSNTS 222

## RESULT 8

Q938P4 PRELIMINARY; PRT; 222 AA.  
 AC Q938P4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Pyrogenic exotoxin A (Fragment).  
 GN SPA.  
 OS Streptococcus equisimilis.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=119602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=4951;  
 RA Kalia A., Bessen D.E.;  
 RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human  
 RT isolates of group G Streptococci";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AV049745; AAL06068.1; .  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005070; F:toxin activity; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR008992; Bact\_endotox.  
 DR InterPro; IPR006177; Bctr1 tox.  
 DR InterPro; IPR006123; Staph/Strep toxin.  
 DR InterPro; IPR006126; Staph/Strep tox.  
 DR InterPro; IPR006173; Staph tox\_OR.  
 DR Pfam; PF01123; Staph\_Strep\_toxin; 1.  
 DR Pfam; PF02876; Staph\_Strep\_tox\_C; 1.  
 DR PRINTS; PR00279; BACTRLTOXIN.  
 DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 FT NON\_TER 1  
 FT NON\_TER 222  
 FT SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 85.8%; Score 1011; DB 2; Length 222;  
 Best Local Similarity 89.2%; Pred. No. 1.4e-66;  
 Matches 189; Conservative 12; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 QDDPSPQLHRSLVKNLQNIYFLVGGDPVTHENVKSVVDQLSHLLIYVNSGPNYDKLKT 60  
 DB 11 QDDPSPQLHRSLVKNLQNIYFLVGGDPVTHENVKSVVDQLSHLLIYVNSGPNYDKLKT 70  
 QY 61 ELKNQEMATLFDKKNVDIYGVYHYLVCYLCEAERSACIYGGVTHNHNHLEIPKIVK 120  
 DB 71 ELKNREMTLFLKKNVDIYGVYHYLVCYLCEAERSACIYGGVTHNHNHLEIPKIVK 130  
 QY 121 VSIDGQSLSFDIETNKQVTAQLDYKVKYLTQNKQLYTNGPSKYETGYIKFIPKNKE 180  
 DB 131 VSIDGQSLSFDIETNKQVTAQLDYKVKYLTQNKQLYTNGPSKYETGYIKFIPKNKE 190  
 QY 181 SFWDFPFPPEFTQSKYLMYKDNETLDSNTS 212  
 DB 191 TFWDFPFPPEFTQSKYLMYKDNETLDSNTS 222

## RESULT 9

Q53678 PRELIMINARY; PRT; 239 AA.  
 AC Q53678;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Enterotoxin (Fragment).  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94011313; PubMed=8406814;  
 RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;  
 RT "Characterization of novel type C staphylococcal enterotoxins:  
 RT biological and evolutionary implications.";  
 RL Infect. Immun. 61:4254-4262 (1993).  
 DR EMBL: I13376; AAA26620.1; .  
 DR HSSP; P34071; ISE2.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0015070; F:toxin activity; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR008992; Bact\_endotox.  
 DR InterPro; IPR006177; Bctr1 tox.  
 DR InterPro; IPR006123; Staph/Strep toxin.  
 DR InterPro; IPR006126; Staph/Strep tox.  
 DR InterPro; IPR006173; Staph tox\_OR.  
 DR Pfam; PF01123; Staph\_Strep\_toxin; 1.  
 DR Pfam; PF02876; Staph\_Strep\_tox\_C; 1.  
 DR PRINTS; PR00279; BACTRLTOXIN.  
 DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 FT NON\_TER 1  
 FT SEQUENCE 239 AA; 27618 MW; A13E7E25C6989C2 CRC64;

Query Match 46.6%; Score 549; DB 2; Length 239;  
 Best Local Similarity 47.2%; Pred. No. 1.1e-32;  
 Matches 111; Conservative 44; Mismatches 66; Indels 14; Gaps 6;  
 QY 1 QDDPSPQLHRSLVKNLQNIYFLVGGDPVTHENVKSVVDQLSHLLIYVNSGPNYDKLKT 56  
 DB 3 QDDPSPQLHRSLVKNLQNIYFLVGGDPVTHENVKSVVDQLSHLLIYVNSGPNYDKLKT 62  
 QY 57 KLKTELKNOEMATLFDKKNVDIYGVYHYLVCYLCEAERSACIYGGVTHNHNHLEIPKIVK 110  
 DB 63 KVKTELLNEDLAKYKDEVDVYGSVYNYCYFSSKDNVGVTKGTVMYGGITKEGHNH 122  
 QY 111 LEIPK--KIVKVSIDGQSLSFDIETNKQVTAQLDYKVKYLTQNKQLYTNGPSKYE 168  
 DB 123 FDNGKLQNLIRVYENKRNITISFEVQTKSKVTAQLDYKVKYLTQNKQLYTNGPSKYE 182  
 QY 169 TGIKFTIPKNKESFDFPPEFTQSKYLMYKDNETLDSNTSQTQIEVYLTK 221  
 DB 183 TGIKFTIENNGNFWYDMWPAQDKFDQSKYLMYKDNETLDSNTSQTQIEVYLTK 237

RESULT 10  
 ID Q9F0L6 PRELIMINARY; PRT; 271 AA.  
 AC Q9F0L6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Staphylococcal enterotoxin C-bovine.  
 GN SEC-BOV.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20566668; PubMed=11114901;  
 RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,  
 RA Meaney W.J., Smyth C.J.;  
 RT "Characterization of a putative pathogenicity island from bovine  
 RT Staphylococcus aureus encoding multiple superantigens";  
 RL J. Bacteriol. 183:63-70 (2001).  
 DR EMBL; AF217235; AAG29599.1; .  
 DR HSSP; P34071; ISE2.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0015070; F:toxin activity; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR008992; Bact\_endotox.  
 DR InterPro; IPR006177; Bctr1 tox.  
 DR InterPro; IPR006123; Staph/Strep toxin.

InterPro; IPR006126; Staph/Strep toxin.  
DR InterPro; IPR006173; Staph toxin OB.  
DR Pfam; PF01123; Staph Strep toxin; 1.  
DR Pfam; PF02876; Staph Strep toxin; 1.  
DR PRINTS; PR00279; BACTRLTOXIN.  
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.  
DR PROSITE; PS00278; STAPH STREP TOXIN 2; 1.  
SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;  
Query Match 46.6%; Score 549; DB 2; Length 271;  
Best Local Similarity 47.2%; Pred. No. 1.3e-32;  
Matches 111; Conservative 44; Mismatches 66; Indels 14; Gaps 6;  
Qy 1 QQDPSPQLHRSSLVKXL-QNYFLYEGDPVTHENVKSDQLSHLLIYVSG---PNYD 56  
Db 35 QPDPTDELKASFTGLMKNMKNLYDDRYVYATKVKSVDFKLAHDLIYNISDKLKNYD 94  
Qy 57 KLKTELKQEMATLFDKKNVDIYGVYHLCYLC--ENAEER---SACIYGGVTHNEGHN 110  
Db 95 KVKTELLNEDLAKKYDEVDVYGSNYVNCYFSSKDNVGVKGTGKTCMYGGITKEGHN 154  
Qy 111 LEIPK--KIVVVKVSDIGIQLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYE 168  
Db 155 FDNGKLQNLVLRVYENKNTISFEVQTDKKSVTQAELDIKARNFLNKNLYEFNSSPYE 214  
Qy 169 TGYIKFIPKNKESFWDFFPEP--EFTQSKYLMYKDNETLDSNTSOIEVYLTTK 221  
Db 215 TGYIKFIENNGNTFWYDMNPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHLTTK 269  
RESULT 11  
Q06532 PRELIMINARY; PRT; 239 AA.  
AC Q06532;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DE Enterotoxin (Fragment).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
ON NCBI\_TaxID=1280;  
RN [1]  
RC SEQUENCE FROM N.A.  
RX MEDLINE=94011313; PubMed=8406814;  
RA Mart J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;  
RT "Characterization of novel type C staphylococcal enterotoxins:  
RL biological and evolutionary implications."  
RL Infect. Immun. 61:4254-4262(1993).  
DR EMBL; L13375; AAA26619.1; -.  
DR HSP; P34071; ISE2.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0015070; F:toxin activity; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR008992; Bact\_endotox.  
DR InterPro; IPR006177; Bctr1 tox.  
DR InterPro; IPR006123; Staph/Strep toxin.  
DR InterPro; IPR006126; Staph/Strep toxin.  
DR Pfam; PF01123; Staph Strep toxin; 1.  
DR Pfam; PF02876; Staph Strep toxin; 1.  
DR PRINTS; PR00279; BACTRLTOXIN.  
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.  
DR PROSITE; PS00278; STAPH STREP TOXIN 2; 1.  
DR NON\_TER 1  
SQ SEQUENCE 239 AA; 27642 MW; C77009F46B8C8D645 CRC64;  
Query Match 46.5%; Score 548; DB 2; Length 239;  
Best Local Similarity 47.2%; Pred. No. 1.3e-32;  
Matches 111; Conservative 43; Mismatches 67; Indels 14; Gaps 6;  
Qy 1 QQDPSPQLHRSS-LVKNLQNYFLYEGDPVTHENVKSDQLSHLLIYVSG---PNYD 56

Db 3 QPDMPDDLHKSSEFTGTMNMKNLYDDHYVYATKVKSVDFKLAHDLIYNISDKLKNYD 62  
Qy 57 KLKTELKQEMATLFDKKNVDIYGVYHLCYLC--ENAEER---SACIYGGVTHNEGHN 110  
Db 63 KVKTELLNEDLAKKYDEVDVYGSNYVNCYFSSKDNVGVKGTGKTCMYGGITKEGHN 122  
Qy 111 LEIP--KIVVVKVSDIGIQLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYE 168  
Db 123 FDNGKLQNLVLRVYENKNTISFEVQTDKKSVTQAELDIKARNFLNKNLYEFNSSPYE 182  
Qy 169 TGYIKFIPKNKESFWDFFPEP--EFTQSKYLMYKDNETLDSNTSOIEVYLTTK 221  
Db 183 TGYIKFIENNGNTFWYDMNPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHLTTK 237  
RESULT 12  
Q06533 PRELIMINARY; PRT; 239 AA.  
AC Q06533;  
DT 01-NOV-1996 (TREMELrel. 01, Created)  
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
DE Enterotoxin (Fragment).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
ON NCBI\_TaxID=1280;  
RN [1]  
RC SEQUENCE FROM N.A.  
RX STRAIN=MNCopeland;  
RX MEDLINE=94011313; PubMed=8406814;  
RA Mart J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;  
RT "Characterization of novel type C staphylococcal enterotoxins:  
RL biological and evolutionary implications."  
RL Infect. Immun. 61:4254-4262(1993).  
DR EMBL; L13378; AAA26622.1; -.  
DR HSP; P34071; ISE.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0015070; F:toxin activity; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR008992; Bact\_endotox.  
DR InterPro; IPR006177; Bctr1 tox.  
DR InterPro; IPR006123; Staph/Strep toxin.  
DR InterPro; IPR006126; Staph/Strep toxin.  
DR Pfam; PF01123; Staph Strep toxin; 1.  
DR Pfam; PF02876; Staph Strep toxin; 1.  
DR PRINTS; PR00279; BACTRLTOXIN.  
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.  
DR PROSITE; PS00278; STAPH STREP TOXIN 2; 1.  
DR NON\_TER 1  
SQ SEQUENCE 239 AA; 27651 MW; A21A95438AE8625 CRC64;  
Query Match 46.4%; Score 547; DB 2; Length 239;  
Best Local Similarity 46.8%; Pred. No. 1.6e-32;  
Matches 110; Conservative 44; Mismatches 67; Indels 14; Gaps 6;  
Qy 1 QQDPSPQLHRSS-LVKNLQNYFLYEGDPVTHENVKSDQLSHLLIYVSG---PNYD 56  
Db 3 QPDPTDELKASSEFTGTMNMKNLYDDHYVYATKVKSVDFKLAHDLIYNISDKLKNYD 62  
Qy 57 KLKTELKQEMATLFDKKNVDIYGVYHLCYLC--ENAEER---SACIYGGVTHNEGHN 110  
Db 63 KVKTELLNEDLAKKYDEVDVYGSNYVNCYFSSKDNVGVKGTGKTCMYGGITKEGHN 122  
Qy 111 LEIP--KIVVVKVSDIGIQLSFDIETNKKMVTQAELDYKVRKYLTDNKQLYTNGPSKYE 168  
Db 123 FDNGKLQNLVLRVYENKNTISFEVQTDKKSVTQAELDIKARNFLNKNLYEFNSSPYE 182  
Qy 169 TGYIKFIPKNKESFWDFFPEP--EFTQSKYLMYKDNETLDSNTSOIEVYLTTK 221  
Db 183 TGYIKFIENNGNTFWYDMNPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHLTTK 237

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RESULT 13
Q8XKJ6 PRELIMINARY; PRT; 266 AA.
AC Q8XKJ6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin type C precursor.
GN SEQ4 OR MW0759.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=136620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR GO; GO:0005576; B:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR008177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph/Strep_toxin; 1.
DR Pfam; PF02876; Staph/Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 46.4%; Score 547; DB 16; Length 266;
Best Local Similarity 46.8%; Pred. No. 1.9e-32;
Matches 110; Conservative 44; Mismatches 67; Indels 14; Gaps 6;

QY 1 QQDPPSQHRRS-LVKNLQNIYFLYEGDPVTHENVKSVQDQLSHLIYVSG---PNTD 56
DB 30 QPDPPELHKSSFTGTGMNKLKYDDHYVSATKVKSVDFKLAHDLIYNI SDKKLKNYD 89
QY 57 KLKTELKNQEMATLFDKKNVDIYGVYHLCYLC--ENAE-----SACIYGGVTNHEGNN 110
DB 90 KVKTELLNEDLAKKYXDEVVDVYGSNYVNCYFSSKDNVGVKGTGKTCMYGGITKEGNN 149
QY 111 LEIP--KKIVVKSIDIGSLSDIETNKKWYTAQELDYKVKYLTNDKQLYTNGSPSKYE 168
DB 150 PDNGNLQNLVIRYVENKRNITISPDVQTKSVTAQELDIKARNFLINKNLYEFNSSPYE 209
QY 169 TGYIKFIPKPKESFWDFPPEP--EFTQSKYLMYKDNETLDSNTSQIEVYLTTK 221
DB 210 TGYIKFIENNGNTFWYDMWPAFGDKPQSKYLMYNDKNTVDSKVKIEVHLTTK 264

RESULT 14
Q05157 PRELIMINARY; PRT; 239 AA.
AC Q05157;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type C enterotoxin (fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=95-011195;

Query Match 46.3%; Score 546; DB 2; Length 239;
Best Local Similarity 47.7%; Pred. No. 1.9e-32;
Matches 112; Conservative 41; Mismatches 68; Indels 14; Gaps 6;

QY 1 QQDPPSQHRRS-LVKNLQNIYFLYEGDPVTHENVKSVQDQLSHLIYVSG---PNTD 56
DB 3 QPDPPELHKSSFTGTGMNKLKYDDHYVSATKVKSVDFKLAHDLIYNI SDKKLKNYD 62
QY 57 KLKTELKNQEMATLFDKKNVDIYGVYHLCYLC--ENAE-----SACIYGGVTNHEGNN 110
DB 63 KVKTELLNEDLAKKYXDEVVDVYGSNYVNCYFSSKDNVGVKGTGKTCMYGGITKEGNN 122
QY 111 LEIP--KKIVVKSIDIGSLSDIETNKKWYTAQELDYKVKYLTNDKQLYTNGSPSKYE 168
DB 123 PDNGNLQNLVIRYVENKRNITISPDVQTKSVTAQELDIKARNFLINKNLYEFNSSPYE 182
QY 169 TGYIKFIPKPKESFWDFPPEP--EFTQSKYLMYKDNETLDSNTSQIEVYLTTK 221
DB 183 TGYIKFIENNGNTFWYDMWPAFGDKPQSKYLMYNDKNTVDSKVKIEVHLTTK 237

RESULT 15
Q06531 PRELIMINARY; PRT; 239 AA.
AC Q06531;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin (fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=4446;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins;
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13374; AAA26618.1; -
DR HSSP; P34071; ISE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
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DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 46.3%; Score 546; DB 2; Length 239;
Best Local Similarity 47.2%; Pred. No. 1.9e-32;
Matches 111; Conservative 43; Mismatches 67; Indels 14; Gaps 6;

Qy 1 QQDDPPSQLRSS-LVKNLQNIYFLYEGDPVTHENVKSVQDLSSHLLIYNVSG---PNYD 56
Db ||| ||| ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 3 QPDMPDPLHKSSFTGTGMNMYLYDDHYVSATKVKSVDFLAHDLIYNISDKRLKNYD 62
Db ||| ||| ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 57 KLKTELKNOEMATLFKDKNVDIYGVYHLCYLC--ENAEER---SACIYGGVTNHEGNH 110
Db ||| ||| ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 63 KVKTELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVGVGKTCMYGGITKHEGNH 122
Db ||| ||| ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 111 LEIP--KKIVVKSIDGIQSLSPDIETNKKAVTAQELDYKVKYLTDNKQLYTNGPSKYE 168
Db : : : ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 123 PDGNLQNLVVRVYENKRNITISFEVQDKKSVTAQELDIKARNFLINKKNLYEFNSSPYE 182
Db : : : ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 169 TGYIKFIPKNKESFWDFDFREP--EFTQSKYLMYKDNETLDSNTSOIEVYLATK 221
Db ||| ||| ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 183 TGYIKFIENNNGNITFYDMMFAPGDKFDQSKYLMYNDKTVDSKSVKIEVHLATK 237
Db ||| ||| ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
```

Search completed: May 7, 2004, 12:09:08  
Job time : 49 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 12:00:52 ; Search time 60 Seconds  
(without alignments)  
1040.717 Million cell updates/sec

Title: US-10-625-221-14

Perfect score: 1178  
Sequence: 1 QQDPSPQLHRSSLVKLNQ.....KDNETLDSNTSQIEVLYLTK 221

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	100.0	251	2 AAW12097	Aaw12097 Streptococ
2	1178	100.0	251	2 AAW59780	Aaw59780 Amino aci
3	1175	99.7	251	2 AAW12154	Aaw12154 Streptoco
4	1174	99.7	251	2 AAW12146	Aaw12146 Streptoco
5	1173	99.6	251	2 AAW12150	Aaw12150 Streptoco
6	1173	99.6	251	2 AAW12147	Aaw12147 Streptoco
7	1169	99.2	221	4 AAB67344	Aab67344 Streptoco
8	1169	99.2	251	2 AAW12148	Aaw12148 Streptoco
9	1168	99.2	251	2 AAW12153	Aaw12153 Streptoco
10	1168	99.2	251	2 AAW12151	Aaw12151 Streptoco
11	1168	99.2	251	2 AAW12152	Aaw12152 Streptoco
12	1164	98.8	251	7 ABU62400	Abu62400 Streptoco
13	1163	98.7	221	2 AAR13209	Aar13209 Streptoco
14	1163	98.7	221	2 AAR45017	Aar45017 Streptoco
15	1163	98.7	221	5 AAB76240	Aab76240 Staphyloc
16	1163	98.7	251	2 AAW12149	Aaw12149 Streptoco
17	1163	98.7	251	2 AAW59798	Aaw59798 Amino aci
18	1163	98.7	251	2 AAW59781	Aaw59781 Amino aci
19	1163	98.7	251	3 AAY70109	Aay70109 Streptoco
20	1163	98.7	251	5 ABB79508	Abb79508 Streptoco
21	1163	98.7	251	6 ABU10088	Abu10088 Streptoco
22	1163	98.7	251	7 ABU62331	Abu62331 Streptoco
23	1163	98.7	251	7 AAE37683	Aae37683 Streptoco
24	1158.5	98.3	250	2 AAW12145	Aaw12145 Streptoco
25	1122	95.2	220	7 ABU62334	Abu62334 Streptoco

26	1122	95.2	220	7 AAE37687	Aae37687 Streptoco
27	1122	95.2	468	7 ABU62335	Abu62335 SPEA L42R
28	1122	95.2	468	7 AAE37684	Aae37684 Streptoco
29	1117	94.8	220	7 AAE37689	Aae37689 S. pyogen
30	1116	94.7	220	7 AAE37688	Aae37688 S. pyogen
31	1116	94.7	468	7 AAE37691	Aae37691 S. pyogen
32	978.5	83.1	250	6 ABU79074	Abu79074 S. pyogen
33	574	48.7	239	2 AAW64647	Aaw64647 Synthetic
34	572	48.6	239	4 AAB67341	Aab67341 Staphyloc
35	572	48.6	255	2 AAW06737	Aaw06737 Staphyloc
36	572	48.6	266	6 ABU79069	Abu79069 S. aureus
37	570	48.4	266	3 AAY92319	Aay92319 Plant-opt
38	563	47.8	286	5 ABB79503	Abb79503 Staphyloc
39	563	47.8	286	7 ABU10083	Abu10083 Staphyloc
40	563	47.8	266	7 AAB62326	Aab62326 S. aureus
41	563	47.8	266	7 AAE37678	Aae37678 Protein #
42	560	47.5	239	5 ABB76237	Abb76237 Staphyloc
43	560	47.5	266	7 ABU62453	Abu62453 S. aureus
44	559	47.5	239	2 AAR13206	Aar13206 Staphyloc
45	559	47.5	239	2 AAR45014	Aar45014 Staphyloc

#### ALIGNMENTS

RESULT 1  
AAW12097  
ID AAW12097 standard; protein; 251 AA.  
XX  
AC AAW12097;  
XX  
DT 04-NOV-1997 (first entry)  
XX  
DE Streptococcus pyogenes Streptococcal toxin A.

Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;  
protection; treatment; cancer; neutralising antibody;  
streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;  
hypotension; group A streptococcal infection; myositis; fascitis;  
liver damage; T cell; lymphoma; ovarian; uterine.

Streptococcus pyogenes.

Key	Location/Qualifiers
Peptide	1..30
Peptide	/label= sig_peptide
Peptide	31..251
Peptide	/label= mat_peptide

W09640930-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US010252.

07-JUN-1995; 95US-00480261.

(MINU) UNIV MINNESOTA.

Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

WPI; 1997-099936/09.

N-PSDB; AAW12097.

Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.

Disclosure; Page 77-79; 102pp; English.

The present sequence is Streptococcus pyogenes Streptococcal toxin A (SPE-A), from which a non-lethal mutant SPE-A, comprising at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce

CC vaccines to protect animals against wild type SPE-A and to treat cancer  
CC and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes  
CC neutralising antibodies (Ab) to be produced, which may be used to  
CC ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal  
CC infection, myositis, fascitis and liver damage. The neutralising Ab is  
CC preferably administered in conjunction with antibiotic therapy. The  
CC mutant SPE-A is especially useful for treating T cell lymphomas, and  
CC ovarian and uterine cancer. It is thought that mutant SPE-A can be  
CC selectively toxic to T cell lymphoma cells  
XX  
SQ Sequence 251 AA;

Query Match 100.0%; Score 1178; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 8.3e-101;  
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QQDPDPSQLHSSLVKQNLQNIYFLYEGDPVTHENVKSDQLLSHLLIYVSGPNYDKLKT 60  
DB 31 QQDPDPSQLHSSLVKQNLQNIYFLYEGDPVTHENVKSDQLLSHLLIYVSGPNYDKLKT 90  
QY 61 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKKIVVK 120  
DB 91 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKKIVVK 150  
QY 121 VSIDGIQSLSDIETNKKQWTAQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180  
DB 151 VSIDGIQSLSDIETNKKQWTAQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 210  
QY 181 SFWFDFPEPEFTQSKYLMYKDNETLDSNTSQIEVILTTK 221  
DB 211 SFWFDFPEPEFTQSKYLMYKDNETLDSNTSQIEVILTTK 251

RESULT 2  
AAWS9780  
ID AAW59780 standard; protein; 251 AA.  
XX  
AC AAW59780;  
XX  
DT 12-OCT-1998 (first entry)  
XX  
DE Amino acid sequence of Streptococcus pyogenes exotoxin A.  
XX  
KW SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;  
KW wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;  
KW streptococcal toxic shock syndrome; STSS; T cell lymphoma;  
KW uterine cancer.  
XX  
OS Streptococcus pyogenes.  
XX  
PN WO9824911-A2.  
XX  
PD 11-JUN-1998.  
XX  
PF 05-DEC-1997; 97WO-US022228.  
XX  
PR 06-DEC-1996; 96US-0032930P.  
XX  
PA (MINU ) UNIV MINNESOTA.  
XX  
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;  
XX  
DR WPI; 1998-333330/29.  
DR N-PSDB; AAW41593.  
XX  
PT New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or  
PT treatment of streptococcal infection or toxic shock syndrome.  
XX  
PS Disclosure; Fig 3; 95pp; English.  
XX  
CC This is the amino acid sequence of the Streptococcus pyogenes exotoxin A  
CC (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least 1  
CC aa change and is nonlethal compared with a protein to wild type SPE-A

CC toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies  
CC that neutralise wild type SPE-A toxin activity. The toxins can be used in  
CC vaccines and therapeutics to generate a protective immune response  
CC against streptococcal infection. They can be used to protect against the  
CC development of streptococcal toxic shock syndrome (STSS). In addition,  
CC the toxins can be used for treating animals with symptoms of  
CC streptococcal infection or STSS and in methods for stimulating T cell  
CC proliferation and in the treatment of cancer. In particular they can be  
CC used for treating T cell lymphomas, and ovarian and uterine cancer  
XX  
SQ Sequence 251 AA;

Query Match 100.0%; Score 1178; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 8.3e-101;  
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QQDPDPSQLHSSLVKQNLQNIYFLYEGDPVTHENVKSDQLLSHLLIYVSGPNYDKLKT 60  
DB 31 QQDPDPSQLHSSLVKQNLQNIYFLYEGDPVTHENVKSDQLLSHLLIYVSGPNYDKLKT 90  
QY 61 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKKIVVK 120  
DB 91 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGHNLEIPKKIVVK 150  
QY 121 VSIDGIQSLSDIETNKKQWTAQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 180  
DB 151 VSIDGIQSLSDIETNKKQWTAQELDYKVRKYLTDNKQLYTNGSPSKYETGYIKFIPKNKE 210  
QY 181 SFWFDFPEPEFTQSKYLMYKDNETLDSNTSQIEVILTTK 221  
DB 211 SFWFDFPEPEFTQSKYLMYKDNETLDSNTSQIEVILTTK 251

RESULT 3  
AAW12154  
ID AAW12154 standard; protein; 251 AA.  
XX  
AC AAW12154;  
XX  
DT 04-NOV-1997 (first entry)  
XX  
DE Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.  
XX  
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;  
KW protection; treatment; cancer; neutralising antibody;  
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;  
KW hypotension; group A streptococcal infection; myositis; fascitis;  
KW liver damage; T cell; lymphoma; ovarian; uterine.  
XX  
OS Streptococcus pyogenes.  
XX  
PN Synthetic.  
XX  
PD Key Location/Qualifiers  
XX Peptide 1..30  
XX /label= sig\_peptide  
XX Peptide 31..251  
XX /label= mat\_peptide  
XX Misc-difference 225  
XX /note= "wild type Ser replaced by Ala"  
XX  
XX WO9640930-A1.  
XX  
XX 19-DEC-1996.  
XX  
XX 07-JUN-1996; 96WO-US010252.  
XX  
XX 07-JUN-1995; 95US-00480261.  
XX  
XX (MINU ) UNIV MINNESOTA.  
XX  
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;  
XX  
XX WPI; 1997-099936/09.  
XX  
DR



XX Mutant SPE-A toxin with at least one amino acid change is substantially  
PT non-lethal - used in vaccine composition for treatment of cancer and  
PT streptococcal toxic shock syndrome etc.  
XX  
XX  
PS Example 4; Page; 102pp; English.  
XX  
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal  
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect  
CC animals against wild type SPE-A and to treat cancer and streptococcal  
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising  
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS  
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,  
CC myositis, fasciitis and liver damage. The neutralising Ab is preferably  
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is  
CC especially useful for treating T cell lymphomas, and ovarian and uterine  
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T  
CC cell lymphoma cells. N.B. Sequence not given in the specification, but  
CC constructed using the wild type SPE-A sequence given on pages 77-79  
XX  
XX Sequence 251 AA;  
XX  
XX Query Match 99.7%; Score 1175; DB 2; Length 251;  
XX Best Local Similarity 99.5%; Pred. No. 1.6e-100;  
XX Matches 220; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 QODPPSOLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHLLIYVSGPNYDKLKT 60  
XX Db 31 QODPPSOLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHLLIYVSGPNYDKLKT 90  
XX  
XX 61 ELKQEMATLFDKKNVDIYGVYHLYCNCNAERSACIYGGVTNHEGNHLEIPKIVVK 120  
XX Db 91 ELKQEMATLFDKKNVDIYGVYHLYCNCNAERSACIYGGVTNHEGNHLEIPKIVVK 150  
XX  
XX 121 VSIDGIQSLSDIETNKKMVTAGELDYKVKYLTDNKQLYTNGPSKYETGVIKFPKNKE 180  
XX Db 151 VSIDGIQSLSDIETNKKMVTAGELDYKVKYLTDNKQLYTNGPSKYETGVIKFPKNKE 210  
XX  
XX 181 SFWDFPFPEFTQSKYLMYKDNELTDSNTSQIEVYLTK 221  
XX Db 211 SFWDFPFPEFTQSKYLMYKDNELTDSNTSQIEVYLTK 251  
XX  
XX RESULT 4  
XX AAW12146  
XX ID AAW12146 standard; protein; 251 AA.  
XX  
XX AC AAW12146;  
XX  
XX DT 04-NOV-1997 (first entry)  
XX  
XX DE Streptococcus pyogenes Streptococcal toxin A mutant Lys157Glu.  
XX  
XX KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;  
XX protection; treatment; cancer; neutralising antibody;  
XX streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;  
XX hypotension; group A streptococcal infection; myositis; fasciitis;  
XX liver damage; T cell; lymphoma; ovarian; uterine.  
XX  
XX OS Streptococcus pyogenes.  
XX Synthetic.  
XX  
XX PH Key Location/Qualifiers  
XX FT Peptide 1..30 /label= sig\_peptide  
XX FT Peptide 31..251 /label= mat\_peptide  
XX FT Misc-difference 187 /note= "wild type Lys replaced by Glu"  
XX  
XX PN WO9640930-A1.  
XX  
XX PD 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010252.  
XX 07-JUN-1995; 95US-00480261.  
XX  
XX (MINU ) UNIV MINNESOTA.  
XX  
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;  
XX WPI; 1997-099936/09.  
XX  
XX Mutant SPE-A toxin with at least one amino acid change is substantially  
PT non-lethal - used in vaccine composition for treatment of cancer and  
PT streptococcal toxic shock syndrome etc.  
XX  
XX Claim 5; Page; 102pp; English.  
XX  
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal  
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect  
CC animals against wild type SPE-A and to treat cancer and streptococcal  
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising  
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS  
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,  
CC myositis, fasciitis and liver damage. The neutralising Ab is preferably  
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is  
CC especially useful for treating T cell lymphomas, and ovarian and uterine  
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T  
CC cell lymphoma cells. N.B. Sequence not given in the specification, but  
CC constructed using the wild type SPE-A sequence given on pages 77-79  
XX  
XX Sequence 251 AA;  
XX  
XX Query Match 99.7%; Score 1174; DB 2; Length 251;  
XX Best Local Similarity 99.5%; Pred. No. 1.9e-100;  
XX Matches 220; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 QODPPSOLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHLLIYVSGPNYDKLKT 60  
XX Db 31 QODPPSOLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHLLIYVSGPNYDKLKT 90  
XX  
XX 61 ELKQEMATLFDKKNVDIYGVYHLYCNCNAERSACIYGGVTNHEGNHLEIPKIVVK 120  
XX Db 91 ELKQEMATLFDKKNVDIYGVYHLYCNCNAERSACIYGGVTNHEGNHLEIPKIVVK 150  
XX  
XX 121 VSIDGIQSLSDIETNKKMVTAGELDYKVKYLTDNKQLYTNGPSKYETGVIKFPKNKE 180  
XX Db 151 VSIDGIQSLSDIETNKKMVTAGELDYKVKYLTDNKQLYTNGPSKYETGVIKFPKNKE 210  
XX  
XX 181 SFWDFPFPEFTQSKYLMYKDNELTDSNTSQIEVYLTK 221  
XX Db 211 SFWDFPFPEFTQSKYLMYKDNELTDSNTSQIEVYLTK 251  
XX  
XX RESULT 5  
XX AAW12150  
XX ID AAW12150 standard; protein; 251 AA.  
XX  
XX AC AAW12150;  
XX  
XX DT 04-NOV-1997 (first entry)  
XX  
XX DE Streptococcus pyogenes Streptococcal toxin A mutant Lys16Asn.  
XX  
XX KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;  
XX protection; treatment; cancer; neutralising antibody;  
XX streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;  
XX hypotension; group A streptococcal infection; myositis; fasciitis;  
XX liver damage; T cell; lymphoma; ovarian; uterine.  
XX  
XX OS Streptococcus pyogenes.  
XX Synthetic.  
XX  
XX PH Key Location/Qualifiers

FT Peptide 1..30  
FT /label= sig\_peptide  
FT Peptide 31..251  
FT /label= mat\_peptide  
FT Misc-difference 46  
FT /note= "wild type Lys replaced by Asn"

XX WO9640930-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010252.

XX 07-JUN-1995; 95US-00480261.

XX (MINU ) UNIV MINNESOTA.

XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

XX WPI; 1997-099936/09.

XX Mutant SPE-A toxin with at least one amino acid change is substantially  
PT non-lethal - used in vaccine composition for treatment of cancer and  
PT streptococcal toxic shock syndrome etc.

XX Example 4; Page; 102pp; English.

XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal  
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect  
CC animals against wild type SPE-A and to treat cancer and streptococcal  
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising  
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS  
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,  
CC myositis, fasciitis and liver damage. The neutralising Ab is preferably  
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is  
CC especially useful for treating T cell lymphomas, and ovarian and uterine  
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T  
CC cell lymphoma cells. N.B. Sequence not given in the specification, but  
CC constructed using the wild type SPE-A sequence given on pages 77-79

XX Sequence 251 AA;

XX Query Match 99.6%; Score 1173; DB 2; Length 251;

XX Best Local Similarity 99.5%; Pred. No. 2.4e-100;

XX Matches 220; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLLSHLLIYNVSGPNYDKLKT 60

DB 31 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLLSHLLIYNVSGPNYDKLKT 90

QY 61 ELKNQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 120

DB 91 ELKNQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 150

QY 121 VSIDGIQSLSDIETNKKWVTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKKE 180

DB 151 VSIDGIQSLSDIETNKKWVTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKKE 210

QY 181 SFWDFPFPEFTQSKYLMYKDNLTDSNTSQIEVILTTK 221

DB 211 SFWDFPFPEFTQSKYLMYKDNLTDSNTSQIEVILTTK 251

RESULT 6

AAW12147

ID AAW12147 standard; protein; 251 AA.

XX AAW12147;

XX 04-NOV-1997 (first entry)

DE Streptococcus pyogenes Streptococcal toxin A mutant Asn20Aasp.

XX

XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;  
KW protection; treatment; cancer; neutralising antibody;  
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;  
KW hypotension; group A streptococcal infection; myositis; fasciitis;  
KW liver damage; T cell; lymphoma; ovarian; uterine.

XX Streptococcus pyogenes.

OS Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..30

FT /label= sig\_peptide

FT Peptide 31..251

FT /label= mat\_peptide

FT Misc-difference 50

FT /note= "wild type Asn replaced by Asp"

XX WO9640930-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US010252.

XX 07-JUN-1995; 95US-00480261.

XX (MINU ) UNIV MINNESOTA.

XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

XX WPI; 1997-099936/09.

XX Mutant SPE-A toxin with at least one amino acid change is substantially  
PT non-lethal - used in vaccine composition for treatment of cancer and  
PT streptococcal toxic shock syndrome etc.

XX Claim 5; Page; 102pp; English.

XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal  
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect  
CC animals against wild type SPE-A and to treat cancer and streptococcal  
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising  
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS  
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,  
CC myositis, fasciitis and liver damage. The neutralising Ab is preferably  
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is  
CC especially useful for treating T cell lymphomas, and ovarian and uterine  
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T  
CC cell lymphoma cells. N.B. Sequence not given in the specification, but  
CC constructed using the wild type SPE-A sequence given on pages 77-79

XX Sequence 251 AA;

XX Query Match 99.6%; Score 1173; DB 2; Length 251;

XX Best Local Similarity 99.5%; Pred. No. 2.4e-100;

XX Matches 220; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLLSHLLIYNVSGPNYDKLKT 60

DB 31 QODPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLLSHLLIYNVSGPNYDKLKT 90

QY 61 ELKNQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 120

DB 91 ELKNQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVK 150

QY 121 VSIDGIQSLSDIETNKKWVTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKKE 180

DB 151 VSIDGIQSLSDIETNKKWVTAQELDYKVRKYLTDNKLQYNGPSKYETGYIKFIPKKE 210

QY 181 SFWDFPFPEFTQSKYLMYKDNLTDSNTSQIEVILTTK 221

DB 211 SFWDFPFPEFTQSKYLMYKDNLTDSNTSQIEVILTTK 251

RESULT 7  
AAB67344  
ID AAB67344 standard; peptide; 221 AA.  
XX  
AC AAB67344;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Streptococcus pyogenes toxin A protein.  
XX  
KW Tumour; cancer; immune; enterotoxin.  
XX  
OS Streptococcus pyogenes.  
XX  
PN US6180097-B1.  
XX  
PD 30-OCT-1998; 98US-00183437.  
XX  
PF 30-OCT-1998;  
XX  
PR 03-OCT-1998; 89US-00416530.  
XX  
PR 17-JAN-1990; 90US-00466577.  
XX  
PR 17-JAN-1991; 91WO-US000342.  
XX  
PR 01-JUN-1992; 92US-00891718.  
XX  
PR 02-MAR-1993; 93US-00025144.  
XX  
PR 31-JAN-1994; 94US-00189424.  
XX  
PR 19-JUN-1995; 95US-00491746.  
XX  
PA (TERM/) Terman D S.  
XX  
PI Terman DS;  
XX  
XX WPI; 2001-158657/16.  
XX  
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or  
PT in vivo comprises exogenous nucleic acids encoding a superantigen and a  
PT costimulatory molecule.  
XX  
XX Disclosure; Fig 2; 16pp; English.  
XX  
XX The present invention relates to a tumour cell capable of stimulating  
CC antitumor immune reactivity in vitro or in vivo contains and expresses an  
CC exogenous nucleic acid molecule encoding a superantigen or its active  
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory  
CC molecule that activates T cells in conjunction with an antigenic  
CC stimulus. The invention may be used for cancer therapy by stimulating an  
CC anticancer immune response in vivo or ex vivo  
XX  
SQ Sequence 221 AA;  
Query Match 99.2%; Score 1169; DB 4; Length 221;  
Best Local Similarity 99.5%; Pred. No. 4.8e-100;  
Matches 220; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QODPDSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHLLIYVNSGPNYDKLKT 60  
DB 1 QODPDSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHLLIYVNSGPNYDKLKT 60  
QY 61 ELKQEMATLFDKKNVDIYGVYHLLCYLCENASACIYGGVTHNHNHLEIPKIVVK 120  
DB 61 ELKQEMATLFDKKNVDIYGVYHLLCYLCENASACIYGGVTHNHNHLEIPKIVVK 120  
QY 121 VSIDGTSQSLFDIETNKQVTAQELDYKVRKYLTDNKNQLYTNGPSKYETGYIKFIPKNE 180  
DB 121 VSIDGTSQSLFDIETNKQVTAQELDYKVRKYLTDNKNQLYTNGPSKYETGYIKFIPKNE 180  
QY 181 SFWDFPPEPPEFTQSKYLMYKNDNTSDNTSQTIEVILTTK 221  
DB 181 SFWDFPPEPPEFTQSKYLMYKNDNTSDNTSQTIEVILTTK 221

AAW12148 standard; protein; 251 AA.  
AAW12148;  
04-NOV-1997 (first entry)  
Streptococcus pyogenes Streptococcal toxin A mutant N20D/K157B.  
Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;  
protection; treatment; cancer; neutralising antibody;  
streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;  
hypotension; group A streptococcal infection; myositis; fasciitis;  
liver damage; T cell; lymphoma; ovarian; uterine.  
Streptococcus pyogenes.  
Synthetic.  
Key Location/Qualifiers  
Peptide 1..30  
/label= sig\_peptide  
Peptide 31..251  
/label= mat\_peptide  
Misc-difference 50  
/note= "wild type Asn replaced by Asp"  
Misc-difference 187  
/note= "wild type Lys replaced by Glu"  
WO9640930-A1.  
19-DEC-1996.  
07-JUN-1996; 96WO-US010252.  
07-JUN-1995; 95US-00480261.  
(MINU) UNIV MINNESOTA.  
Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;  
WPI; 1997-099936/09.  
Mutant SPE-A toxin with at least one amino acid change is substantially  
non-lethal - used in vaccine composition for treatment of cancer and  
streptococcal toxic shock syndrome etc.  
Claim 5; Page; 102pp; English.  
The present sequence is a non-lethal Streptococcus pyogenes Streptococcal  
toxin A (SPE-A) mutant, which can be used to produce vaccines to protect  
animals against wild type SPE-A and to treat cancer and streptococcal  
toxic shock syndrome (STSS). The mutant SPE-A causes neutralising  
antibodies (Ab) to be produced, which may be used to ameliorate STSS  
symptoms, e.g. fever, hypotension, group A streptococcal infection,  
myositis, fasciitis and liver damage. The neutralising Ab is preferably  
administered in conjunction with antibiotic therapy. The mutant SPE-A is  
especially useful for treating T cell lymphomas, and ovarian and uterine  
cancer. It is thought that mutant SPE-A can be selectively toxic to T  
cell lymphoma cells. N.B. Sequence not given in the specification, but  
constructed using the wild type SPE-A sequence given on pages 77-79  
Sequence 251 AA;  
Query Match 99.2%; Score 1169; DB 2; Length 251;  
Best Local Similarity 99.1%; Pred. No. 5.7e-100;  
Matches 219; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QODPDSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHLLIYVNSGPNYDKLKT 60  
DB 31 QODPDSQLHRSLSLVKLNQNIYFLYEGDPVTHENVKSVDDLHLLIYVNSGPNYDKLKT 90  
QY 61 ELKQEMATLFDKKNVDIYGVYHLLCYLCENASACIYGGVTHNHNHLEIPKIVVK 120  
DB 91 ELKQEMATLFDKKNVDIYGVYHLLCYLCENASACIYGGVTHNHNHLEIPKIVVK 150

Handwritten notes:  
Cips not prior  
Cips  
Doesn't substantially  
from waspara-gine (N)

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QY 121 VSIDGQSLSFDIETNKKQWTAQBLDYKVRKYLTDNKKQLYTNGSKYETGYIKFIPKNKE 180
DB 151 VSIDGQSLSFDIETNKKQWTAQBLDYKVRKYLTDNKKQLYTNGSKYETGYIKFIPKNKE 210
QY 181 SFWDFPEPEPEFTOSKYLMIYKDNELDSNTSQIEVLITTK 221
DB 211 SFWDFPEPEPEFTOSKYLMIYKDNELDSNTSQIEVLITTK 251

RESULT 9
AAW12153
ID AAW12153 standard; protein; 251 AA.
AC AAW12153;
XX
DT 04-NOV-1997 (first entry)
DE Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fasciitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Peptide /label= sig_peptide
FT Peptide 31..251
FT Peptide /label= mat_peptide
FT Misc-difference 120
FT /note= "wild type Cys replaced by Ser"
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX
DR WPI; 1997-099936/09.
XX
PT Mutant SPE-A toxin with at least one amino acid change is substantially
PT non-lethal - used in vaccine composition for treatment of cancer and
PT streptococcal toxic shock syndrome etc.
XX
PS Example 4; Page; 102pp; English.
XX
CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
CC animals against wild type SPE-A and to treat cancer and streptococcal
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
CC myositis, fasciitis and liver damage. The neutralising Ab is preferably
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and uterine
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
CC cell lymphoma cells. N.B. Sequence not given in the specification, but
CC constructed using the wild type SPE-A sequence given on pages 77-79
XX
SQ Sequence 251 AA;

```

Query Match 99.2%; Score 1168; DB 2; Length 251;

```

Best Local Similarity 99.5%; Pred. No. 7e-100;
Matches 220; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLSHLLIYNVSGPNVDKLT 60
DB 31 QDDPPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLSHLLIYNVSGPNVDKLT 90
QY 61 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIVVK 120
DB 91 ELKNQEMATLFDKKNVDIYGVVEYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIVVK 150
QY 121 VSIDGQSLSFDIETNKKQWTAQBLDYKVRKYLTDNKKQLYTNGSKYETGYIKFIPKNKE 180
DB 151 VSIDGQSLSFDIETNKKQWTAQBLDYKVRKYLTDNKKQLYTNGSKYETGYIKFIPKNKE 210
QY 181 SFWDFPEPEPEFTOSKYLMIYKDNELDSNTSQIEVLITTK 221
DB 211 SFWDFPEPEPEFTOSKYLMIYKDNELDSNTSQIEVLITTK 251

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RESULT 10
AAW12151
ID AAW12151 standard; protein; 251 AA.
AC AAW12151;
XX
DT 04-NOV-1997 (first entry)
DE Streptococcus pyogenes Streptococcal toxin A mutant Cys87Ser.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fasciitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Peptide /label= sig_peptide
FT Peptide 31..251
FT Peptide /label= mat_peptide
FT Misc-difference 117
FT /note= "wild type Cys replaced by Ser"
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX
DR WPI; 1997-099936/09.
XX
PT Mutant SPE-A toxin with at least one amino acid change is substantially
PT non-lethal - used in vaccine composition for treatment of cancer and
PT streptococcal toxic shock syndrome etc.
XX
PS Example 4; Page; 102pp; English.
XX
CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
CC animals against wild type SPE-A and to treat cancer and streptococcal
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
CC myositis, fasciitis and liver damage. The neutralising Ab is preferably
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and uterine
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
CC cell lymphoma cells. N.B. Sequence not given in the specification, but
CC constructed using the wild type SPE-A sequence given on pages 77-79
XX
SQ Sequence 251 AA;

```

CC myositis, fascitis and liver damage. The neutralising Ab is preferably  
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is  
CC especially useful for treating T cell lymphomas, and ovarian and uterine  
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T  
CC cell lymphoma cells. N.B. Sequence not given in the specification, but  
CC constructed using the wild type SPE-A sequence given on pages 77-79  
XX  
SQ Sequence 251 AA;

Query Match 99.2%; Score 1168; DB 2; Length 251;  
Best Local Similarity 99.5%; Pred. No. 7e-100;  
Matches 220; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QQDPSPQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDQLSHHLLIYVSGPNYDKLKT 60  
DB 31 QQDPSPQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDQLSHHLLIYVSGPNYDKLKT 90  
QY 61 ELKQEMATLFDKKNVDIYGVYHLLCYLCENASACIYGGVTHNHNLEIPKIVVK 120  
DB 91 ELKQEMATLFDKKNVDIYGVYHLLCYLCENASACIYGGVTHNHNLEIPKIVVK 150  
QY 121 VSIDGQSLSFDIETNKKWMTAQELDYKVRKYLTONKQLYTNGPSKYETGYIKFIPKKE 180  
DB 151 VSIDGQSLSFDIETNKKWMTAQELDYKVRKYLTONKQLYTNGPSKYETGYIKFIPKKE 210  
QY 181 SFWDFPPEPFTQSKYLMYKDNETLDSNTSQIEVYLTK 221  
DB 211 SFWDFPPEPFTQSKYLMYKDNETLDSNTSQIEVYLTK 251

RESULT 11  
AAW12152  
ID AAW12152 standard; protein; 251 AA.  
XX  
AC AAW12152;  
DT 04-NOV-1997 (first entry)  
XX

Streptococcus pyogenes Streptococcal toxin A mutant Cys98Ser.  
XX  
XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;  
KW protection; treatment; cancer; neutralising antibody;  
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;  
KW hypotension; group A streptococcal infection; myositis; fascitis;  
KW liver damage; T cell; lymphoma; ovarian; uterine.  
XX

Streptococcus pyogenes.  
OS Synthetic.

Key Location/Qualifiers  
FH Peptide 1..30  
FT Peptide /label= sig\_peptide  
FT Peptide 31..251  
FT /label= mat\_peptide  
FT Misc-difference 128  
FT /note= "wild type Cys replaced by Ser"  
XX  
XX WO9640930-A1.  
XX  
XX 19-DEC-1996.  
XX  
XX 07-JUN-1996; 96WO-US010252.  
XX  
XX 07-JUN-1995; 95US-00480261.  
XX  
XX (MINU) UNIV MINNESOTA.  
XX  
XX Schlievert PM, Roggiani M, Stoeck J, Ohlendorf D;  
XX  
XX WPI; 1997-099936/09.  
XX  
XX Mutant SPE-A toxin with at least one amino acid change is substantially  
XX non-lethal - used in vaccine composition for treatment of cancer and

streptococcal toxic shock syndrome etc.  
Example 4; Page; 102pp; English.

The present sequence is a non-lethal Streptococcus pyogenes Streptococcal  
toxin A (SPE-A) mutant, which can be used to produce vaccines to protect  
animals against wild type SPE-A and to treat cancer and streptococcal  
toxic shock syndrome (STSS). The mutant SPE-A causes neutralising  
antibodies (Ab) to be produced, which may be used to ameliorate STSS  
symptoms, e.g. fever, hypotension, group A streptococcal infection,  
myositis, fascitis and liver damage. The neutralising Ab is preferably  
administered in conjunction with antibiotic therapy. The mutant SPE-A is  
especially useful for treating T cell lymphomas, and ovarian and uterine  
cancer. It is thought that mutant SPE-A can be selectively toxic to T  
cell lymphoma cells. N.B. Sequence not given in the specification, but  
constructed using the wild type SPE-A sequence given on pages 77-79  
XX  
SQ Sequence 251 AA;

Query Match 99.2%; Score 1168; DB 2; Length 251;  
Best Local Similarity 99.5%; Pred. No. 7e-100;  
Matches 220; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QQDPSPQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDQLSHHLLIYVSGPNYDKLKT 60  
DB 31 QQDPSPQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDQLSHHLLIYVSGPNYDKLKT 90  
QY 61 ELKQEMATLFDKKNVDIYGVYHLLCYLCENASACIYGGVTHNHNLEIPKIVVK 120  
DB 91 ELKQEMATLFDKKNVDIYGVYHLLCYLCENASACIYGGVTHNHNLEIPKIVVK 150  
QY 121 VSIDGQSLSFDIETNKKWMTAQELDYKVRKYLTONKQLYTNGPSKYETGYIKFIPKKE 180  
DB 151 VSIDGQSLSFDIETNKKWMTAQELDYKVRKYLTONKQLYTNGPSKYETGYIKFIPKKE 210  
QY 181 SFWDFPPEPFTQSKYLMYKDNETLDSNTSQIEVYLTK 221  
DB 211 SFWDFPPEPFTQSKYLMYKDNETLDSNTSQIEVYLTK 251

RESULT 12  
ABU62460  
ID ABU62460 standard; protein; 251 AA.  
XX  
AC ABU62460;  
DT 27-AUG-2003 (first entry)  
XX  
DE Streptococcus pyrogenic toxin a L42A mutant.  
XX  
XX SPEa; streptococcus pyrogenic enterotoxin a; mutant; vaccine; mutein;  
KW superantigen toxin; MHC; superantigen-associated bacterial infection;  
KW bacterial infection; antibacterial.  
XX  
OS Streptococcus sp.  
OS Synthetic.

Key Location/Qualifiers  
FH Peptide 1..30  
FT Peptide /label= Signal\_peptide  
FT Protein 31..251  
FT /label= Mature\_SPEa\_L42R  
FT Misc-difference 72  
FT /note= "Wild-type Leu substituted by Ala"  
XX  
XX US2003036644-A1.  
XX  
XX 20-FEB-2003.  
XX  
XX 26-NOV-2001; 2001US-00002784.  
XX  
XX 25-JUN-1997; 97US-00882431.  
XX  
XX 01-SEP-1998; 98US-00144776.

*Handwritten signature*

XX PA (ULRI/ ) ULRICH R G.  
XX FI Ulrich RG;  
XX DR WPI; 2003-492125/46.  
XX PT New superantigen toxin DNA fragment, useful for preparing a composition  
XX PT for treating or preventing bacterial infection.  
XX FS Example 13; Page; 69pp; English.  
XX CC The invention relates to an isolated and purified superantigen toxin DNA  
XX CC fragment is altered so that binding of the encoded altered toxin to  
XX CC either the MHC class II or T cell antigen receptor is altered. Also  
XX CC included are a recombinant DNA construct (comprising a vector and an  
XX CC isolated and purified altered superantigen toxin DNA fragment), a host  
XX CC cell transformed with the recombinant DNA construct, producing altered  
XX CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)  
XX CC superantigen toxin peptide, diagnosing superantigen-associated bacterial  
XX CC infection, a vaccine (comprising an altered superantigen toxin for  
XX CC producing antigenic and immunogenic response resulting in the protection  
XX CC of a mammal against superantigen-associated bacterial infection),  
XX CC treating/ameliorating a superantigen-associated bacterial infection, an  
XX CC antiserum isolated from individuals immunised with one or more altered  
XX CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-  
XX CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,  
XX CC SEB, SEC1) and streptococcal pyrogenic enterotoxin A and b (SPEa and  
XX CC SPEb). The superantigen toxin DNA fragment is useful for preparing a  
XX CC composition for treating or preventing bacterial infection. The present  
XX CC mutant of SPEa. Note: The present sequence is not shown in the  
XX CC specification but was created by the indexer using the wild-type sequence  
XX CC and the information in the specification  
XX SQ Sequence 251 AA;

Query Match 98.8%; Score 1164; DB 7; Length 251;  
Best Local Similarity 99.1%; Pred. No. 1.6e-99;  
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QDDPPSOLHRSGLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYNVSGPNYDKLT 60  
Db 31 QDDPPSOLHRSGLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYNVSGPNYDKLT 90  
QY 61 ELKNQEMATLFDKKNVDIYGVYHLYLVCENASACIYGGVTNHEGHNLEIPKIVVK 120  
Db 91 ELKNQEMATLFDKKNVDIYGVYHLYLVCENASACIYGGVTNHEGHNLEIPKIVVK 150  
QY 121 VSIDGQSLSFDIETNKKMTAQELDYKVRKYLTDNKKLYTNGPSKYETGYIKFIPKNKE 180  
Db 151 VSIDGQSLSFDIETNKKMTAQELDYKVRKYLTDNKKLYTNGPSKYETGYIKFIPKNKE 210  
QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 221  
Db 211 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 251

RESULT 13  
AAR13209  
ID AAR13209 standard; protein; 221 AA.  
XX AC AAR13209;  
XX DT 27-AUG-2003 (revised)  
XX DT 15-OCT-1991 (first entry)  
XX DE Streptococcal pyrogenic enterotoxin A.  
XX KW SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.  
XX OS Streptococcus sp.

PN WO9110680-A.  
XX PD 25-JUL-1991.  
XX PF 17-JAN-1990; 90US-00466577.  
XX PR 17-JAN-1990; 90US-00466577.  
XX PA (TERM/) TERMAN D S.  
XX PI Terman DS;  
XX DR WPI; 1991-237984/32.  
XX CC Treating cancer with enterotoxin from Staphylococcus aureus -  
XX CC administered by IV injection, having same tumoricidal activity as  
XX CC Staphylococcal protein A without potential toxic reactions.  
XX PS Disclosure; Fig 1; 74pp; English.  
XX CC SPE A can be used for tumoricidal treatment, esp. with a haemolysin.  
XX CC Synthetic polypeptides having structural homology to Streptococcal  
XX CC pyrogenic exotoxins are claimed, provided the homology includes  
XX CC statistically significant sequence homology, alignment of Cysteine  
XX CC residues and similar hydrophathy profiles. See AAR13203-R13211. (Updated  
XX CC on 27-AUG-2003 to correct OS field.)  
XX SQ Sequence 221 AA;  
Query Match 98.7%; Score 1163; DB 2; Length 221;  
Best Local Similarity 99.1%; Pred. No. 1.7e-99;  
Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 QDDPPSOLHRSGLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYNVSGPNYDKLT 60  
Db 1 QDDPPSOLHRSGLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYNVSGPNYDKLT 60  
QY 61 ELKNQEMATLFDKKNVDIYGVYHLYLVCENASACIYGGVTNHEGHNLEIPKIVVK 120  
Db 61 ELKNQEMATLFDKKNVDIYGVYHLYLVCENASACIYGGVTNHEGHNLEIPKIVVK 120  
QY 121 VSIDGQSLSFDIETNKKMTAQELDYKVRKYLTDNKKLYTNGPSKYETGYIKFIPKNKE 180  
Db 121 VSIDGQSLSFDIETNKKMTAQELDYKVRKYLTDNKKLYTNGPSKYETGYIKFIPKNKE 180  
QY 181 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 221  
Db 181 SFWDFPFPEFTQSKYLMYKDNETLDSNTSQIEVYLTTK 221

RESULT 14  
AAR45017  
ID AAR45017 standard; protein; 221 AA.  
XX AC AAR45017;  
XX DT 25-MAR-2003 (revised)  
XX DT 08-JUN-1994 (first entry)  
XX DE Staphylococcal enterotoxin SPE A.  
XX KW Staphylococcal enterotoxin; SE; cancer; tumouricide; agent;  
XX KW autoimmune disease; toxicity; Protein A; perfusion system.  
XX OS Staphylococcus aureus.  
XX PN WO9324136-A1.  
XX PD 09-DEC-1993.  
XX PF 01-JUN-1993; 93WO-US005213.  
XX PF 01-JUN-1992; 92US-00891718.

asp acid  
e position  
45  
Not  
separagme  
(N)

XX (TERM/) Terman D S.  
PA (STON/) STONE J L.  
XX Terman DS, Stone JL;  
XX WPI; 1993-405418/50.  
XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer  
XX in a patient or for the treatment of auto-immune diseases.  
XX Disclosure; Fig 1; 90pp; English.  
XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)  
XX which may be used in the methods of the invention for treating cancer in  
XX a patient. These SEs, and homologues of them, can be used as tumouricidal  
XX agents for treating cancers and autoimmune disease. They exhibit  
XX tumouricidal activity and toxicity identical to that observed for the  
XX Protein A perfusion system. They may be administered by i.v. injection.  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX Sequence 221 AA;  
XX  
XX Query Match 98.7%; Score 1163; DB 2; Length 221;  
XX Best Local Similarity 99.1%; Pred. No. 1.7e-99;  
XX Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX QY 1 QQDPSPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDDLHSHLIYVSGPNYDKLKT 60  
XX Db 1 QQDPSPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDDLHSHLIYVSGPNYDKLKT 60  
XX  
XX QY 61 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTHHEGHNHLEIPKIVVK 120  
XX Db 61 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTHHEGHNHLEIPKIVVK 120  
XX  
XX QY 121 VSDIGIQLSFDIETNKKMTAQELDYKVKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180  
XX Db 121 VSDIGIQLSFDIETNKKMTAQELDYKVKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180  
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XX QY 181 SFWDFPPEPFTQSKYLMYKDNFTLDSNTSQIEVYLTK 221  
XX Db 181 SFWDFPPEPFTQSKYLMYKDNFTLDSNTSQIEVYLTK 221  
XX  
XX RESULT 15  
XX ID ABB76240  
XX AC ABB76240 standard; protein; 221 AA.  
XX DT 09-AUG-2002 (first entry)  
XX DE Staphylococcus pyogenes exotoxin A.  
XX EX Exotoxin A; SPE A; superantigen; antigen; tumour; cancer; antitumour;  
XX KW therapy.  
XX OS Streptococcus pyogenes.  
XX PN US2002051765-A1.  
XX PD 02-MAY-2002.  
XX PF 19-DEC-2000; 2000US-00741503.  
XX PR 03-OCT-1989; 89US-00416530.  
XX PR 17-JAN-1990; 90US-00466577.  
XX PR 17-JAN-1991; 91WO-US000342.  
XX PR 01-JUN-1992; 92US-00891718.  
XX PR 02-MAR-1993; 93US-00025144.  
XX PR 31-JAN-1994; 94US-00189424.  
XX PR 19-JUN-1995; 95US-00491746.  
XX

XX (TERM/) Terman D S.  
PA Terman DS;  
XX WPI; 2002-415198/44.  
XX Reagent for treating cancer without the need for e.g. radiotherapy,  
XX comprises a specific V beta subset of T cells sensitized to a growing  
XX tumor and stimulated with superantigens.  
XX Disclosure; Fig 2; 17pp; English.  
XX The present sequence is the protein sequence of exotoxin A (SPE A) of  
XX Streptococcus pyogenes. Similarity is shown, in several stretches of  
XX sequence, between staphylococcal enterotoxins, streptococcal pyrogenic  
XX exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the  
XX present invention, synthetic polypeptides useful in tumour therapy and in  
XX blocking or destroying autoreactive T and B lymphocyte populations are  
XX characterised by substantial structural homology to staphylococcal  
XX enterotoxin A and enterotoxin B, and to streptococcal pyrogenic  
XX exotoxins, with statistically significant sequence homology and  
XX similarity (Z value of Lipman and Pearson algorithm in Monte Carlo  
XX analysis exceeding 6) to include alignment of cysteine residues and  
XX similar hydropathy profiles. These superantigens are used to treat solid  
XX tumours, including their metastases, without radiation, surgery or  
XX standard chemotherapeutic agents. A claimed method of human cancer  
XX treatment involves contacting haematopoietic cells from a patient with  
XX one or more superantigens ex vivo to generate stimulated cells, selecting  
XX a specific V beta subset of cells, and reintroducing these cells into the  
XX patient to induce an in vivo therapeutic, tumouricidal reaction  
XX  
XX Sequence 221 AA;  
XX  
XX Query Match 98.7%; Score 1163; DB 5; Length 221;  
XX Best Local Similarity 99.1%; Pred. No. 1.7e-99;  
XX Matches 219; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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XX Db 1 QQDPSPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDDLHSHLIYVSGPNYDKLKT 60  
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XX QY 61 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTHHEGHNHLEIPKIVVK 120  
XX Db 61 ELKQEMATLFDKKNVDIYGVYHLCYLCEAERSACIYGGVTHHEGHNHLEIPKIVVK 120  
XX  
XX QY 121 VSDIGIQLSFDIETNKKMTAQELDYKVKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180  
XX Db 121 VSDIGIQLSFDIETNKKMTAQELDYKVKYLTDNKQLYTNGPSKYETGYIKFIPKNKE 180  
XX  
XX QY 181 SFWDFPPEPFTQSKYLMYKDNFTLDSNTSQIEVYLTK 221  
XX Db 181 SFWDFPPEPFTQSKYLMYKDNFTLDSNTSQIEVYLTK 221  
XX  
XX Search completed: May 7, 2004, 12:07:38  
XX Job time : 62 secs

NO POSTING

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2004, 06:36:07 ; Search time 4334 Seconds  
(without alignments)  
12753.783 Million cell updates/sec

Title: US-10-625-221-12  
Perfect score: 1851  
Sequence: 1 ccatcacgacatcatgt.....ttagcaactattttatgc 1851

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_in:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rtd:\*
- 26: em\_gss\_pug:\*
- 27: em\_gss\_vrt:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	97	5.2	1200	13	BX415878
C 2	96.8	5.2	1200	13	BX437758
C 3	96.2	5.2	1277	28	CC253231
C 4	93.8	5.1	1101	29	CNS0039G

C 5	91.6	4.9	1200	13	BX437739
C 6	91.4	4.9	1201	13	BX355654
C 7	91.2	4.9	1201	13	BX443774
C 8	90.2	4.9	1202	23	CC262481
C 9	89.8	4.9	1124	13	BX436282
C 10	89.8	4.9	1201	9	AL565455
C 11	89.6	4.8	1201	13	BX446296
C 12	88.8	4.8	1201	9	AL565455
C 13	88.4	4.8	1101	29	CNS0039G
C 14	87.8	4.7	1101	29	CNS0039G
C 15	87.8	4.7	1201	9	AL536104
C 16	87.8	4.7	1201	13	BX437779
C 17	86.8	4.7	1201	13	BX458623
C 18	86.6	4.7	1896	29	CG753083
C 19	86.4	4.7	1056	13	BX415058
C 20	86.4	4.7	1592	29	CG750135
C 21	86.2	4.7	945	29	CNS040DK
C 22	86.2	4.7	1200	13	BX437758
C 23	86.2	4.7	1201	9	AL536104
C 24	85.8	4.6	1101	29	CNS0006J
C 25	85.2	4.6	1101	29	CNS0006J
C 26	85.2	4.6	1200	13	BX415878
C 27	85	4.6	1099	13	BX456575
C 28	84.8	4.6	1187	28	B11102
C 29	84.6	4.6	1201	13	BX420717
C 30	83.2	4.5	1101	29	CNS003BD
C 31	82	4.4	961	29	CNS008HI
C 32	81.6	4.4	639	29	CNS017QD
C 33	81.4	4.4	899	13	BX453223
C 34	81.2	4.4	1201	13	BX355642
C 35	80.8	4.4	1056	13	BX415058
C 36	80	4.3	1076	13	BX338020
C 37	80	4.3	1391	29	CG754863
C 38	79.4	4.3	1001	29	CNS0064G
C 39	79.4	4.3	1204	29	CNS016E2
C 40	79.2	4.3	1101	29	CNS003B4
C 41	79.2	4.3	1101	29	CNS016LI
C 42	79	4.3	1044	13	BX415231
C 43	78.8	4.3	646	14	CF547155
C 44	78.8	4.3	987	29	CNS014FQ
C 45	78.8	4.3	1200	13	BX437739

ALIGNMENTS

RESULT 1

BX415878/c  
LOCUS BX415878 Homo sapiens THYMUS Homo sapiens cdna clone CS0CAP008Y104  
DEFINITION 5-PRIME, mRNA sequence.  
ACCESSION BX415878  
VERSION BX415878.1 GI:30765550  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1200)  
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
Bp 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/InvitroGen Corporation 1600 Paraday Avenue Genoscope sequence ID: CS0CAP008B802QP1.

FEATURES

Location/Qualifiers  
1..1200  
/organism="Homo sapiens"







BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION  
AL063921  
VERSION  
AL063921.1  
KEYWORDS  
GSS.  
SOURCE  
Drosophila melanogaster (fruit fly)  
ORGANISM  
Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Mecoptera; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source

1..1101  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR08K10"  
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/note="end : TET3"

ORIGIN

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Best Local Similarity 18.3%; Pred. No. 2.5e-05;  
Matches 123; Conservative 287; Mismatches 261; Indels 0; Gaps 0;

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DB 421 WAAAAATAATTWAAWAAAAAATTTWAAAAAATAAAWATATWTTTATWAAAAA 480  
QY 141 CAATCGCAATTGATGACATTCGACATTCGAACTAAATTCATCAATTTGTTACTAACACAACTA 200  
DB 481 AATTWTTTTTTTATTTATTTATATATTTTATATTTTAAWAAAAAATAAAWAAAAWATA 540  
QY 201 GATTGACAACTAATTTCTCAACAAACGTTAATTTTAAACAACTAAGTAACTCCACCCAGC 260  
DB 541 AATTWTTTWTWTTTWTWAAWATAAAWAAWYHTTWTWYHTTWTWYHTTWTWYHTT 600  
QY 261 TCCATCAATGCTACGTAAGTAATCATCACTACTTAACTTAACTTCTTACATCAAGTTT 320  
DB 601 AWAHTTWTWYHTTAAWHTTWTWAAWHTTWTWAAWHTTWTWAAWHTTWTWAAWHTT 660  
QY 321 TTCTTTTGTCTGTGTTGATGAGTACCACTTCTATATATTTATGACAACTAAATTCAC 380  
DB 661 AAATWTTTWTWYHTTAAWYHTTWTWYHTTWTWYHTTWTWYHTTWTWYHTTWTWY 720  
QY 381 AACTCTCAATTTATTTTCTGCTACTCAAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 440  
DB 721 HYMYMYWYMYWYMYWYMYWYMYWYMYWYMYWYMYWYMYWYMYWYMYWYMYWYMY 780  
QY 441 ACCATCACTTCTCACTCTCTCTACCGTCACAACTTCTCATCTCTCACTTCTCTGTT 500  
DB 781 WATTHYHTTTHYHTTTHYHTTTHYHTTTHYHTTTHYHTTTHYHTTTHYHTTTHYHT 840

QY 501 GGTAACACATATCAATATCTTCCGTTTTCAGCACTATCGTACTGTGTCTACCTAAA 560  
DB 841 HHTTWWHTTTHWHTTWTWHTTWTWHTTWTWHTTWTWHTTWTWHTTWTWHTTWTWHTT 900  
QY 561 ATATACCCCTTATCAATCACTTCTTTAAACATCATATATATAACATATTTCTACCTCT 620  
DB 901 HHTTTCMCHHMTCTCHHHTTWTWHTTCHHHTTWTWHTTCHHHTTWTWHTTCHHHTT 960  
QY 621 ACCTATCTATCGTAAAGATAAATAAATACTATTTGTTTCTTATTTTATTAATAATA 680  
DB 961 HHCCHHHTTTHHHTTTHHHTTTHHHTTTHHHTTTHHHTTTHHHTTTHHHTTTHHHTT 1020  
QY 681 ATTATTAATATAAGTTAATATGTTTAAAAAATATAACAATTTTATTTCTATTTATAGT 740  
DB 1021 ATTTTWWHTTTHWHTTWTWHTTWTWHTTWTWHTTWTWHTTWTWHTTWTWHTTWTW 1080  
QY 741 TATTTTTCAT 751  
DB 1081 HHHHTTTHHHTTTHHHTTTHHHTTTHHHTTTHHHTTTHHHTTTHHHTTTHHHTT 1091  
RESULT 5  
BX437739/c  
LOCUS  
DEFINITION  
BX437739 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YG24  
3-PRIME, mRNA sequence.  
ACCESSION  
BX437739  
VERSION  
BX437739.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1200)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 534.r For  
more information about this cluster, see  
<http://www.genoscope.cns.fr/>  
cgi-bin/cluster.cgi?seq=CS0CAP008BD12NP1&cluster=534.r. Contact :  
Feng Liang Email : fliang@life.com URL :  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
Paraday Avenue Genoscope sequence ID : CS0CAP008BD12NP1.  
FEATURES  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="CS0CAP008YG24"  
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
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double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

ORIGIN

Query Match 4.9%; Score 91.6; DB 13; Length 1200;  
Best Local Similarity 37.4%; Pred. No. 5.3e-05;  
Matches 301; Conservative 110; Mismatches 387; Indels 6; Gaps 3;

QY 343 TTACCAATACTTCTTATATATTGACAACTAAATTCACAACTCTTCAATATTTTCTGT 402  
DB 1196 TTTTMMHHTTATTCMTTHTTATHTTHTTHTTHTTHTTHTTHTTHTTHTTHTTHTT 1137  
QY 403 CTACTCAAAGTTTCTTCTTATGATAGTCTAATTCACCACTACTTCTTCCACTCTCT 462



DEFINITION BX43774 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA clone CS0DH007YF12 5-PRIME, mRNA sequence.

ACCESSION BX43774

VERSION BX43774.1 GI:30772178

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Chukayorta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jesse, J., and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)

AUTHORS

TITLE

JOURNAL

COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 131 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7885.f For more information about this cluster, see <http://www.genoscope.cns.fr/>  
cgi-bin/cluster.cgi?seq=CS0DH007DC06QPI&cluster=7885.f. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DH007DC06QPI.  
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FEATURES  
source

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Qy	647	ATAACTATGTTTTTTTTGGTTATTTTATAAAAAATTTAATAATAAGITTAATGTTTTTT	706
Db	1091	ATTATATWTWTWTWTWTWTWTATATTAABAATAATATTTTTTTWAIAAAAAAAAAA	1032
Qy	707	AAAAATATACA-----ATTTTATCTATTTTATAGTAGCTATTTTTTCATTGTAGTAA	760
Db	1031	AAAWATATATATATATATATTTWTWTWTATTAAMWTATATAAAAAATTTTTAAABAWATAW	972
Qy	761	TATTGGTGAAATGTAATAACCTTTTTTAATCTAGAGGAGAACCCAGATATAAAATGGAGG	820
Db	971	ATWTWTWTAAWTAAWATAAATAAAWWMAWMTWTATTTTTTWAAWMTATATATTTT	912
Qy	821	AATATTAATGAAACAATAAAAAAGTAGTATCGAAGAAATGGTATTTTTTGGTTTTAGTGAC	880
Db	911	TATATAATAAAAAAANAANWWTWTWTWTAAAAAANAATATTTWTWTWTWTAT	852
Qy	881	ATTTCTCGACTAACATCTCGCAGAGGTATTTGCTCAACAGACGCCGATCCAAGCCA	940
Db	851	AWAWATATATAAAAAAANAANWTTTWTATAAANAANAATAANTWTWTATTTT	792
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Db	731	TT 673
Qy	1061	TAATGTTTCAGGCCCAATTTATGATAAATTAATAAACTGAACCTTAAGAACCAAGAGATGCC 1120
Db	672	TANWAKGKGGDWAAA 613
Qy	1121	AACTTTATTAAAGATAAAACGTTTGATATTTATGGTGTAGAATATTACCATCTCTGTTA 1180
Db	612	AA 553
Qy	1181	TTTATGTGAAATGCAGAAAGGAG 1204
Db	552	TTTATTGAACATGTTATAAAGAG 529
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CC262481/c		
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DEFINITION	CH261-167M9_Sp6.1 CH261 Gallus gallus genomic clone CH261-167M9,	
	genomic survey sequence.	
ACCESSION	CC262481	
VERSION	CC262481.1	GI:30607397
KEYWORDS	GSS.	
SOURCE	Gallus gallus (chicken)	
ORGANISM	Gallus gallus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	
	Phasianinae; Gallus.	
REFERENCE	1 (bases 1 to 1202)	
AUTHORS	Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,	
	Warren,W., Graves,T., Mardis,E. and Wilson,R.	
TITLE	Gallus gallus BAC End Reads	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: Richard K. Wilson	
	Genome Sequencing Center	
	Washington University School of Medicine	
	Email: submissions@watson.wustl.edu	
	Insert Length: 182000 Std Error: 0.00	
	Seq primer: Sp6 ATTAGGTGACACTATAG	
	Class: BAC ends	
	High quality sequence start: 30	
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	CH261 Female Chicken library - for library and clone	
	ordering information: http://www.chori.org/bacpac"	
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Best Local Similarity	44.5%;	Fried.No. 8.7e-05;
Matches 408; Conservative	0;	Mismatches 498; Indels 10; Gaps 3
Qy	558	AAAAATATACCCCTTATCAATCGCTTCTTTAAACTCATCTATATATAACATATTTTCATCT 617
Db	1109	AAATTTTATATAAAAAATAAAATAATTAATAATTTTATATTTTATTTTATTTTAAAAAT 105
Qy	618	CTACTATCTATTCGTAAAGATAAAATAAATCACTATTGTTTTTTTGTATTATTAAT 677
Db	1049	AAATATATAAATAATAATAAAAAATAAATAATTAATAAATAATTTATATTTTAAATAT 990
Qy	678	AAAAATTTAATATAAGTTAATGTTTTTTTTTAAAAAATATACAATTTTATCTTATTAAGTT 737



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RESULT 10
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DEFINITION AL565455 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CSODF005YO18 3-PRIME, mRNA sequence.
ACCESSION AL565455
VERSION AL565455.2 GI:30549492
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12916848.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF005BH09NP1&cluster=9232.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF005BH09NP1.
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Location/Qualifiers
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
ORIGIN
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Best Local Similarity 32.4%; Pred. No. 0.0001;
Matches 243; Conservative 135; Mismatches 372; Indels 1; Gaps 1;
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QY 704 TTTAAAAATATACAAATTTATTTCTATTTATAGTTAGTATTTTTCATTTGTAGTAATAT 763
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QY 764 TGGTGAATGTGAATACCTTTTAAATCTAGGGAGACCCAGATATAAATGAGGAAT 823
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DB 1095 TAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATAWATA 1154
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LOCUS
DEFINITION BX446296 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
XCL0BB001ZA03 3-PRIME, mRNA sequence.
ACCESSION BX446296
VERSION BX446296.1 GI:30784407
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : XCL0BB001ZA03FP1.
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Location/Qualifiers
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo (dT) primer. Five prime end enriched,
double-strand cDNA was digested with NotI and cloned into
the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 4.8%; Score 89.6; DB 13; Length 1201;
Best Local Similarity 35.8%; Pred. No. 0.00011;
Matches 194; Conservative 87; Mismatches 261; Indels 0; Gaps 0;
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DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL063921

VERSION AL063921.1 GI:4941778

KEYWORDS Drosophila melanogaster (fruit fly)

SOURCE Drosophila melanogaster

ORGANISM Drosophila melanogaster

REFERENCE 1 (bases 1 to 1101)

AUTHORS Aaron Mammeter in Pister de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES

source

1. 1101

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/clone="BACR08K10"

/clone\_lib="RPCI-98"

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ORIGIN

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Best Local Similarity 20.3%; Pred. No. 0.00017;

Matches 146; Conservative 295; Mismatches 269; Indels 8; Gaps 2;

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1040 WMTWATWDTWWDKWWWATAKTDTMTWRTAWRWDAGDRGAGKRRDADTDAGA 981

946 ACAGATCTAGTTAGTTAAACCTTCAAAATATATATTTTCTTTATGAGGGTGACCTG 1005

980 GRDGGGRKEKKDRKGDDKGGKGGKKAAGKATKWDMDWMDWMDWMDGAKRKA 921

1006 TTACTCAGAGATGTGAATCTGTGATCACTTTTATCTCACCATTATATATATATG 1065

920 DDDGAGDKDDGKGDADDTTGTGDKDDDKDDKDDKDDKAGTGTGATWAAATDWWWG 861

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860 WAD-----ADWTTWDAADWDADRDWDAWAKWDDAWAGARTADRRWDGAGKRG 808

1126 TATTTAAGATAAAGCTGTGATTTATTTGTTGTAGATATATACCATCTCTCTTTATAT 1185

807 GAKRRDRKRDADKRDADDAADAAATTTTTRDTRDTRDTRDTRDTRDTRDTRDTRD 748

1186 GTGAAATGCAAGAAAGAGTGCATGATCTACGAGGGGTAAACAATCATGAGGGAATC 1245

747 DDDDRDRAGTAGRKWRRTWKRWRKRTDTRDADADTADDRDRRREGDGDAGAGKGTG 688

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DB 627 WKANDWAKWMDKTRADRWDRWAADTTWDARADRWAKARAWARRDRRAARADRWTT 568

QY 1366 GAAAATATCTTACAGATAAAGCAACTATATATATAATGAGCCTCTTAATAATGAAACTG 1425

DB 567 KGKTTTATTTWAAARAWAWAWATTTATTTT-TWTTTWTTTTWTTTTWTTTTAAW 509

QY 1426 GATATATAAGCTTCATACCTAAGATAAAGAAAGTTTGGTTTGTGATTTTCCCTGAAC 1485

DB 508 AAWTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 449

QY 1486 CAGATTTTACTCAATCTAATAATCTTATGATATAAAGATAATGAACGCTGACTC 1543

DB 448 TWAATTTTWTWTTTAAATAATTTTWTWTTTAAATAAATAAATAAATAAATAAATAA 391

CNS000EVL 1101 bp DNA linear GSS 04-JUN-1999

Drosophila melanogaster genome survey sequence T7 end of BAC:

BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL069706

AL069706.1 GI:4949849

GSS.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

Genoscope.

1 (bases 1 to 1101)

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammeter in Pister de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES

source

1. 1101

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

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/clone\_lib="RPCI-98"

/note="end : T7"

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Best Local Similarity 34.9%; Pred. No. 0.00021;

Matches 221; Conservative 122; Mismatches 284; Indels 6; Gaps 3;

QY 476 TTATCATCTCTCACTTTTTCGTTGGTGATACATATCAATATCTTCGTTTACG 535



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 10:40:02 ; Search time 7000 Seconds  
(without alignments)  
11461.137 Million cell updates/sec

Title: US-10-625-221-12  
Perfect score: 1  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sta.\*  
12: gb\_sy.\*  
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14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
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22: em\_ov.\*  
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29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
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39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1835.4	99.2	1837	6	AR089274 Sequence
4	1835.4	99.2	1837	6	AR093474 Sequence
5	1832.2	99.0	1837	6	AR211577 Sequence
6	1832.2	99.0	1837	6	BD223209 Bacterial
7	1830.6	98.9	1837	6	AX800046 Sequence
8	1668.4	90.1	4621	7	SPU40453
9	1406.6	76.0	57506	1	AE014161
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11	1225.4	66.2	11900	1	AE009982
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13	754.4	40.8	756	6	AX110260
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37	566.2	30.6	667	1	AY049745
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39	310.6	16.8	311650	1	AF005144
40	299	16.2	9220	1	AE010048
41	295.2	15.9	310950	1	AF005143
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ALIGNMENTS

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LOCUS	AR408359	Sequence 12 from patent US 6632441.			
DEFINITION	AR408359				
ACCESSION	AR408359.1	GI:40158507			
VERSION	AR408359.1				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1851)				
AUTHORS	Schlievert, P.M., Roggiani, M., Stoehr, J. and Ohlendorf, D.				
TITLE	Mutants of streptococcal toxin a and methods of use				
JOURNAL	Patent: US 6632441-A 12 14-OCT-2003;				
FEATURES	Location/Qualifiers				

appdians

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QY	1561	AACTCTACCTAACCAACCAAGTAACTTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTT 1620	
DB	1561	AACTCTACCTAACCAACCAAGTAACTTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTT 1620	
QY	1621	AGAAATTTTATGCAATTTCTTTTATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1680	
DB	1621	AGAAATTTTATGCAATTTCTTTTATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1680	
QY	1681	TCTTATCTAAAGGAGCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGGAATTTTGTGA 1740	
DB	1681	TCTTATCTAAAGGAGCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGGAATTTTGTGA 1740	
QY	1741	TTTGTCTATTTGATGAGGTAATCCCATTTTTCGACAGACATCGTGTGCACTCT 1800	
DB	1741	TTTGTCTATTTGATGAGGTAATCCCATTTTTCGACAGACATCGTGTGCACTCT 1800	
QY	1801	AACACCAAAATCATAGACAGGAGCTTGTAGCTTAGCAACTATTTTATCGTC 1851	
DB	1801	AACACCAAAATCATAGACAGGAGCTTGTAGCTTAGCAACTATTTTATCGTC 1851	

RESULT 2  
 BD063209  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 unclassified  
 1 (bases 1 to 1851)  
 Schlievert, P.M., Roggiani, M., Stoeck, J. and Ohlendorf, D.

BD063209  
 Mutants of streptococcal toxin A and methods of use.  
 BD063209.1  
 GI:22608812  
 JP 2001505439-A/12.  
 unclassified  
 unclassified  
 1 (bases 1 to 1851)  
 Schlievert, P.M., Roggiani, M., Stoeck, J. and Ohlendorf, D.



QY 1801 AACACCAAAATCATAGACAGAGCTTGTAGCTTAGCAACTATTTTATCGTC 1851  
Db 1801 AACACCAAAATCATAGACAGAGCTTGTAGCTTAGCAACTATTTTATCGTC 1851

RESULT 3  
LOCUS AR089274 1837 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 33 from patent US 5994066.  
ACCESSION AR089274  
VERSION AR089274.1 GI:10016031  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1837)  
Bergeon, M.G.; Picard, P.J.; Ouellette, M. and Roy, P.H.  
Species-specific and universal DNA probes and amplification primers  
to rapidly detect and identify common bacterial pathogens and  
associated antibiotic resistance genes from clinical specimens for  
routine diagnosis in microbiology laboratories  
Patent: US 5994066-A 33 30-NOV-1999;  
FEATURES  
Location/Qualifiers  
1..1837  
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ORIGIN  
Query Match 99.2%; Score 1835.4; DB 6; Length 1837;  
Best Local Similarity 99.9%; Pred. No. 5,6e-254;  
Matches 1836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TCATGTTTGACAGCTTATCATGATGAGCTTACTTTTCGATCAGGTCTATCCTTGAAC 74  
Db 1 TCATGTTTGACAGCTTATCATGATGAGCTTACTTTTCGATCAGGTCTATCCTTGAAC 60  
QY 75 AGGTGCACATAGATTAGGCGATGAGATTTACGACAACTATGAACTATATCTAC 134  
Db 61 AGGTGCACATAGATTAGGCGATGAGATTTACGACAACTATGAACTATATCTAC 120  
QY 135 ATCAGCGAATCGGCAATGATGACATTTGAACTAAATCAATTTGTTTACTAACAG 194  
Db 121 ATCAGCGAATCGGCAATGATGACATTTGAACTAAATCAATTTGTTTACTAACAG 180  
QY 195 CAAGTATGACAACTAATTTCTCAACAACTGTTTAACTTAACTTCAAGTACTCCC 254  
Db 181 CAAGTATGACAACTAATTTCTCAACAACTGTTTAACTTAACTTCAAGTACTCCC 240  
QY 255 ACCAGTCCATCAATGCTTACCGTAACTAATCAATTTTAACTTAACTTCAATCA 314  
Db 241 ACCAGTCCATCAATGCTTACCGTAACTAATCAATTTTAACTTAACTTCAATCA 300  
QY 315 GGTGTTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 374  
Db 301 GGTGTTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 360  
QY 375 ATTGCAACTCTTCAATTTTCTGCTACTCAAAAGTTTCTTCAATTTGATATAGTCT 434  
Db 361 ATTGCAACTCTTCAATTTTCTGCTACTCAAAAGTTTCTTCAATTTGATATAGTCT 420  
QY 435 AATTCCACCATCACTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 494  
Db 421 AATTCCACCATCACTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
QY 495 TCGTGGTGAACACATAAATCAATTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 554  
Db 481 TCGTGGTGAACACATAAATCAATTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 540  
QY 555 CTTAAATATACCCCTTATCAATTCGTTCTTTTAACTCATCTATATATATATTTTCT 614  
Db 541 CTTAAATATACCCCTTATCAATTCGTTCTTTTAACTCATCTATATATATATTTTCT 600  
QY 615 CCTCCTACCTATCTATCGTAAAGATAAAATACTATTGTTTTTTTGTATTTTAT 674

601 CCTCCTACCTATCTATCTGTAAGAGATAAAATAAATAAATAAATAAATAAATAAATAA 660  
QY 675 AATAAATTTAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 734  
Db 661 AATAAATTTAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 720  
QY 735 GTTAGCTATTTTTCATTTAGTAAATTTGTTGTAATTTGTAATTTGTAATTTGTAATTT 794  
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QY 795 AGAGAACCCAGATATAAATCGAGATATAAATCGAGATATAAATCGAGATATAAATCGAG 854  
Db 781 AGAGAACCCAGATATAAATCGAGATATAAATCGAGATATAAATCGAGATATAAATCGAG 840  
QY 855 AAAATGCTATTTTTCATTTAGTAAATTTGTTGTAATTTGTAATTTGTAATTTGTAATTT 914  
Db 841 AAAATGCTATTTTTCATTTAGTAAATTTGTTGTAATTTGTAATTTGTAATTTGTAATTT 900  
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Db 961 AATATATATTTTCTTATGAGGTGACCTGTTTATCTCAGGAGATTTGAAATCTGTTGAT 1020  
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Db 1021 CAATTTTATCTCAACATTTAATAATAAATTTTTCAGGCGCAAAATTTATGATAAATTTAA 1080  
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Db 1081 ACTGAACCTTAAAGAACCAAGATGCGCACTTTTATTTAAGGATAAATAAATTTGATATTT 1140  
QY 1155 GGTGTAGAATTTTACCATCTCTGTTTATTTATGTAATAATTTGTAATAATTTGTAATAAT 1214  
Db 1141 GGTGTAGAATTTTACCATCTCTGTTTATTTATGTAATAATTTGTAATAATTTGTAATAAT 1200  
QY 1215 TAGCGAGGTGAACAAATCATGAGGGAATCATTTAGAAATTTCTTAAAGATGATGCTGTT 1274  
Db 1201 TAGCGAGGTGAACAAATCATGAGGGAATCATTTAGAAATTTCTTAAAGATGATGCTGTT 1260  
QY 1275 AAAAGTATCAATCGATGTTATCCAAAGCTTATCATTTGATTTGAAACAAATAAATAAATG 1334  
Db 1261 AAAAGTATCAATCGATGTTATCCAAAGCTTATCATTTGATTTGAAACAAATAAATAAATG 1320  
QY 1335 GTAACTGCTCAAGAAATTAGACTATTAAGTTAGAAATATCTTACAGATTAATAGCAACTA 1394  
Db 1321 GTAACTGCTCAAGAAATTAGACTATTAAGTTAGAAATATCTTACAGATTAATAGCAACTA 1380  
QY 1395 TATATAATGGAACCTTCTAAATATGAACTGGAATATATAAAGTTTCACTTAAAGATAA 1454  
Db 1381 TATATAATGGAACCTTCTAAATATGAACTGGAATATATAAAGTTTCACTTAAAGATAA 1440  
QY 1455 GAAAGTTTTTGGTTTGGTTTTTCCCTGACCAAGATTTTCTCAATCTTAAATCTTATG 1514  
Db 1441 GAAAGTTTTTGGTTTGGTTTTTCCCTGACCAAGATTTTCTCAATCTTAAATCTTATG 1500  
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Db 1501 ATATATAAGATTAATGAAACGCTTGTACTCAACCAAGCCAAATTTGAAGTCTACCTAAC 1560  
QY 1575 ACCAAGTAACTTTTGGTTTTTGGCAACCTTACCTACCTGCTGGATTTAGAAATTTTATG 1634  
Db 1561 ACCAAGTAACTTTTGGTTTTTGGCAACCTTACCTACCTGCTGGATTTAGAAATTTTATG 1620  
QY 1635 AATCTTTTATTAATGTAAGAAACCGCTCATTTGATGAGCGGTTTTGCTTTATCTAAAGGA 1694  
Db 1621 AATCTTTTATTAATGTAAGAAACCGCTCATTTGATGAGCGGTTTTGCTTTATCTAAAGGA 1680  
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QY 1635 AATCTTTTATTAATGTAATAAACCGCTCATATTGATGAGCGGTTTGTCTTATCTAAAGGA 1694  
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QY 1695 GCTTTACCTCTAATGCTGCAAAATTTTAAAGTTGGATTTTGTATTTTGTCTTATTTGTAT 1754  
Db 1681 GCTTTACCTCTAATGCTGCAAAATTTTAAAGTTGGATTTTGTATTTTGTCTTATTTGTAT 1740  
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Db 1741 TTGATGGGTAAATCCATTTTTCGACAGACATGCTGTCGCCACCTCTTAACACCAAAATCAT 1800  
QY 1815 AGACAGAGCTGTAGCTTACCACTATTTTATCGTC 1851  
Db 1801 AGACAGAGCTGTAGCTTACCACTATTTTATCGTC 1837

RESULT 5  
AR211577  
LOCUS AR211577 1837 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 15 from patent US 6399332.  
ACCESSION AR211577  
VERSION AR211577.1 GI:21514936  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1837)  
AUTHORS Ulrich,R.G., Olson,M.A. and Bavari,S.  
TITLE Bacterial superantigen vaccines  
JOURNAL Patent: US 6399332-A 15 04-JUN-2002;  
FEATURES  
source location/Qualifiers  
1. 1837  
/organism="unknown"  
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ORIGIN  
Query Match 99.0%; Score 1832.2; DB 6; Length 1837;  
Best Local Similarity 99.8%; Pred. No. 1.6e-253;  
Matches 1834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 15 TCATGTTTGACAGCTTATCATCGATAGCTTACCTTTTCGATCAGGCTCATCTTGAAC 74  
Db 1 TCATGTTTGACAGCTTATCATCGATAGCTTACCTTTTCGATCAGGCTCATCTTGAAC 60  
QY 75 AGGTGCAACATAGATTAGGCGATGAGATTTACCAGACAACTATGAACGTATATACCTAC 134  
Db 61 AGGTGCAACATAGATTAGGCGATGAGATTTACCAGACAACTATGAACGTATATACCTAC 120  
QY 135 ATCAGCAATCGGCAATTTGATGACATTTGGAACCTAAATTCATCAATTTGTTTACTAACAG 194  
Db 121 ATCAGCAATCGGCAATTTGATGACATTTGGAACCTAAATTCATCAATTTGTTTACTAACAG 180  
QY 195 CAACCTAGATTGACAACTAAATTTCTCAACAAAGTTAAATTTTAAACAACTCAAGTAACTCCC 254  
Db 181 CAACCTAGATTGACAACTAAATTTCTCAACAAAGTTAAATTTTAAACAACTCAAGTAACTCCC 240  
QY 255 ACCAGCTCATCAATGCTTACGTAAGTAATCATAACTTAACTAAACCTTGTTCATCAACAA 314  
Db 241 ACCAGCTCATCAATGCTTACGTAAGTAATCATAACTTAACTAAACCTTGTTCATCAACAA 300  
QY 315 GGTGTTTTCTTTTCTGTTGTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 374  
Db 301 GGTGTTTTCTTTTCTGTTGTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
QY 375 ATGCAACTCTTCAATTTTCTGCTACTCAAGTTTCTCAAGTTTCTCAAGTTTCTCAAGTTTCTCA 434  
Db 361 ATGCAACTCTTCAATTTTCTGCTACTCAAGTTTCTCAAGTTTCTCAAGTTTCTCAAGTTTCTCA 420  
QY 435 AATTCACCATCAGCTTCTCACTCTCTCACTCTCTCACTCTCTCACTCTCTCACTCTCTCACTCTT 494  
Db 421 AATTCACCATCAGCTTCTCTCACTCTCTCACTCTCTCACTCTCTCACTCTCTCACTCTCTCACTT 480

QY 495 TCGTGTGTAACACATAATCAAAATATCTTTCCGTTTTCACGACTATCGCTACTGTGTCA 554  
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QY 675 AATAAAATTTATTAATTAAGTTTATGTTTTTAAATAATATCAATTTTATTTCTATTTATA 734  
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QY 1395 TATACATAATGGACCTTCTAAATATGAAACTGGATATATAAAGTTTCTATACCTAAGATAA 1454  
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QY 1575 ACCAAGTAATCTTTGCTTTTGGCAACCTTACTACTGCTGGATTTAGAAATTTTATGCT 1634



Db	1561	ACCAAGTAACCTTTTGGCAACCTTACCTACTGCTGGAATTTAGAAATTTATTGC	1620
Qy	1635	AATCTTTTATTAATGTAAGTAAACCGCTCATTTGATGAGCGGTTTGTCTTATCTTAAGGA	1694
Db	1621	AATCTTTTATTAATGTAAGTAAACCGCTCATTTGATGAGCGGTTTGTCTTATCTTAAGGA	1680
Qy	1695	GCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGGATTTTTCGTAATTTGCTATTGAT	1754
Db	1681	GCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGGATTTTTCGTAATTTGCTATTGAT	1740
Qy	1755	TTGATGGGTAATPCCATTTTTCGACAGACATGCTGCGCCCTCTTAACACAAATCAT	1814
Db	1741	TTGATGGGTAATPCCATTTTTCGACAGACATGCTGCGCCCTCTTAACACAAATCAT	1800
Qy	1815	AGACAGGAGCTGTAGCTTAGCAATTTTATTTATCGTC	1851
Db	1801	AGACAGGAGCTGTAGCTTAGCAATTTTATTTATCGTC	1837
RESULT 6	BD232309	1837 bp DNA linear	PAT 17-JUL-2003
LOCUS	BD232309	Bacterial superantigen vaccine.	
DEFINITION	BD232309	Bacterial superantigen vaccine.	
ACCESSION	BD232309		
VERSION	BD232309.1	GI:33032979	
KEYWORDS	JP 2002522055-A/8.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1. (bases 1 to 1837)		
AUTHORS	Ulrich, R.G., Olson, M.A. and Bavari, S.		
TITLE	Bacterial superantigen vaccine		
JOURNAL	Patent: JP 2002522055-A 8 23-JUL-2002;		
COMMENT	WALTER REED ARMY INSTITUTE OF RESEARCH		
	OS Unidentified		
	PN JP 2002522055-A/8		
	PD 23-JUL-2002		
	PF 13-AUG-1998 JP 2000564656		
	PI ROBERT G. ULICH, MARK A. OLSON, SINA BAVARI		
	PC S42N15/00, A61K39/085, A61P31/00, A61P35/00, A61P37/04,		
	PC C07K14/31,		
	PC C12N1/21, C12P21/02, G01N33/53, G01N33/569, C12N15/00 CC		
	Strandedness: Unknown;		
CC	Topology: Unknown;		
CC	Bacterial superantigen vaccine		
PH	Key Location/Qualifiers		
FT	source 1. 1837		
FT	/organism='Unidentified'.		
FEATURES	Location/Qualifiers		
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ORIGIN			
Query Match	99.0%;	Score 1832.2;	DB 6; Length 1837;
Best Local Similarity	99.8%;	Pred. No. 1.6e-253;	
Matches 1834;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
Qy	15	TCATGTTGACAGCTTATCATGATAGCTTATTTTCGAATCAGGTCTATCCCTGAAC	74
Db	1	TCATGTTGACAGCTTATCATGATAGCTTATTTTCGAATCAGGTCTATCCCTGAAC	60
Qy	75	AGGTGCAACATAGATTAGGCGATGGAGATTTCACAGCAACTATGAACGTATATCTAC	134
Db	61	AGGTGCAACATAGATTAGGCGATGGAGATTTCACAGCAACTATGAACGTATATCTAC	120
Qy	135	ATCAGCGCAATCGGCAATTGATGATGCAATTTAAATTTCAATTTGTTTCTTAACAG	194
Db	121	ATCAGCGCAATCGGCAATTGATGATGCAATTTAAATTTCAATTTGTTTCTTAACAG	180
Qy	195	CAACTAGATTGCAACATTAATCTCAACACAGTTTATTTTAAACACATTCAGTAACCTCC	254

Db	181	CAACTAGATTGCAACATTAATCTCAACAAACGTTAATTTAAACAACTTCAAGTAACCTCC	240
Qy	255	ACCAGCTCCATCAATGCTTACCGTAACTAATCACTAATTAATAAAACCTTGTGTACATCA	314
Db	241	ACCAGCTCCATCAATGCTTACCGTAACTAATCACTAATTAATAAAACCTTGTGTACATCA	300
Qy	315	GGTTTTTCTTTTGTCTTGTCTATGAGTTACCAATCTTCTATATTTATTTGACAACTAA	374
Db	301	GGTTTTTCTTTTGTCTTGTCTATGAGTTACCAATCTTCTATATTTATTTGACAACTAA	360
Qy	375	ATTGACAACTCTTCAATTAATTTTCTGCTACTCAAAAGTTTCTTCTATTTGATATAGTCT	434
Db	361	ATTGACAACTCTTCAATTAATTTTCTGCTACTCAAAAGTTTCTTCTATTTGATATAGTCT	420
Qy	435	AATTCCACCATCACTTCTTCCACTCTCTCTACCGTCAACATTTCACTCATCTCTCATCTTT	494
Db	421	AATTCCACCATCACTTCTTCCACTCTCTCTACCGTCAACATTTCACTCATCTCTCATCTTT	480
Qy	495	TCGTGGTGAACACATAATCAATATCTTCCGTTTTCGCTTTTACGCACTATCGCTACTGTGCA	554
Db	481	TCGTGGTGAACACATAATCAATATCTTCCGTTTTCGCTTTTACGCACTATCGCTACTGTGCA	540
Qy	555	CCTAAATATATACCCCTTATCAATCGCTTCTTTTAACTCATCTATATATAACATTTTCAT	614
Db	541	CCTAAATATATACCCCTTATCAATCGCTTCTTTTAACTCATCTATATATAACATTTTCAT	600
Qy	615	CTCTCTACCTATCTATTCGTAAGAAATATAAATACTATTGTTTTTTTGTATTTTAT	674
Db	601	CTCTCTACCTATCTATTCGTAAGAAATATAAATACTATTGTTTTTTTGTATTTTAT	660
Qy	675	AATAAATTTATTAATTAAGTTAATGTTTTTAAATATATACAATTTTATTTATTTATA	734
Db	661	AATAAATTTATTAATTAAGTTAATGTTTTTAAATATATACAATTTTATTTATTTATA	720
Qy	735	GTTAGCTATTTTTCATTTGTTAGTAATATTTGTTGAATTTGTAATAACCTTTTAAATCTAG	794
Db	721	GTTAGCTATTTTTCATTTGTTAGTAATATTTGTTGAATTTGTAATAACCTTTTAAATCTAG	780
Qy	795	AGGAGACCCAGATATAAATGAGGAAATTAATGAAACAAATAAATAAGTATTTCGAAG	854
Db	781	AGGAGACCCAGATATAAATGAGGAAATTAATGAAACAAATAAATAAGTATTTCGAAG	840
Qy	855	AAATGCTATTTTGTGTTTGTGACATTTCTTTGGACTAAACAATCTCGCAAGAGGTATTT	914
Db	841	AAATGCTATTTTGTGTTTGTGACATTTCTTTGGACTAAACAATCTCGCAAGAGGTATTT	900
Qy	915	GCTCAACAGACCCCGATCCAGCCACTTCACAGATCTAGTTTAGTTAAACCTTCAA	974
Db	901	GCTCAACAGACCCCGATCCAGCCACTTCACAGATCTAGTTTAGTTAAACCTTCAA	960
Qy	975	AATATATATTTTCTTTATGAGGTTGACCTGTTTACTCACGAGAAATGTAATCTGTTGAT	1034
Db	961	AATATATATTTTCTTTATGAGGTTGACCTGTTTACTCACGAGAAATGTAATCTGTTGAT	1020
Qy	1035	CAACTTTTCTGACCAATTTAATATAATGTTTCAGGCGCAATTTATGTAATTAATAA	1094
Db	1021	CAACTTTTCTGACCAATTTAATATAATGTTTCAGGCGCAATTTATGTAATTAATAA	1080
Qy	1095	ACTGAATTTAAGAACCAAGAGATGCGCAACTTTTATTTAAGGATATAAAGCTTGTATTTAT	1154
Db	1081	ACTGAATTTAAGAACCAAGAGATGCGCAACTTTTATTTAAGGATATAAAGCTTGTATTTAT	1140
Qy	1155	GGTGTAGAAATTAACCACTCTCTGTTATTTATGTAATAATGCAAGAGAGTGCATGATC	1214
Db	1141	GGTGTAGAAATTAACCACTCTCTGTTATTTATGTAATAATGCAAGAGAGTGCATGATC	1200
Qy	1215	TACGAGGGGTAAACAAATCATGAAGGAATCATTTAGAAATTCCTAAAAAGATAGTCGT	1274
Db	1201	TACGAGGGGTAAACAAATCATGAAGGAATCATTTAGAAATTCCTAAAAAGATAGTCGT	1260
Qy	1275	AAAGTATCAATTCGATGGTATCCAAAGGCTATCATTTGATATGTAATAAATAAATG	1334

Db 1261 AAAGTATCAATCGATCGTATCCAAAGCCTATCATTTTGATATTGAAACAAATAAAAAATG 1320  
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Db 1321 GTAACCTGCTCAAGATTAAGTATTAAGTTAGAAAATATCTTACAGATTAATAGCAACTA 1380  
Qy 1395 TATACCTAATGGACCTTCTAATATGAACCTGGATATATAAAGTTTATACCTAAGATAAAA 1454  
Db 1381 TATACCTAATGGACCTTCTAATATGAACCTGGATATATAAAGTTTATACCTAAGATAAAA 1440  
Qy 1455 GAAAGTTTTGGTTTGATTTTTTCCCTGGAACCAAGAAATTTACTCAATCTAAATATCTTATG 1514  
Db 1441 GAAAGTTTTGGTTTGATTTTTTCCCTGGAACCAAGAAATTTACTCAATCTAAATATCTTATG 1500  
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RESULT 7  
AX800046 1837 bp DNA linear PAT 13-OCT-2003  
LOCUS Sequence 15 from Patent WO03056015.  
DEFINITION AX800046  
ACCESSION AX800046  
VERSION AX800046.1 GI:37653325  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1  
AUTHORS Ulrich, R.G.  
TITLE Bacterial superantigen vaccines  
JOURNAL Patent: WO 03056015-A 5 10-JUL-2003;  
U.S. Medical Research Institute of Infectious Diseases (US)  
Location/Qualifiers  
1. 1837  
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/note="streptococcal pyrogenic exotoxin-A mutant"

FEATURES source  
ORIGIN  
Query Match 98.9%; Score 1830.6; DB 6; Length 1837;  
Best Local Similarity 99.8%; Pred. No. 2.7e-253;  
Matches 1833; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 15 TCATGTTTGACAGCTTATCATCGATAAGCTTACCTTTTCGATCAGGCTCATCTTGAAC 74  
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Qy 75 AGGTGCAACATAGATTAGGGCATGAGATTTTACCAGACCACTATGAAAGGTATATCTAC 134  
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Db	1261	AAAGTATCAATCGATGATCCAAAGCCTATCATTTGATATTTGAAACAAATAAAAAATG	1320
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QY	1695	GCTTTACCTCTTAATGCTCAAAATTTTAAAGTTGATTTTGTCTATCTATGAT	1754
Db	1681	GCTTTACCTCTTAATGCTCAAAATTTTAAAGTTGATTTTGTCTATCTATGAT	1740
QY	1755	TTGATCGGTAATCCCAATTTTGCACAGACATCGTCTGCGACCTCTTAACACCAAAATCAT	1814
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QY	1815	AGACAGAGCTTGTAGCTTAGCAACTATTTTATCGTC	1851
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RESULT 8	SPU40453	4621 bp DNA linear PHG 11-MAR-1997	
LOCUS		Streptococcus pyogenes phage T12 repressor, excisionase (xis),	
DEFINITION		integrate (int) and erythrogenic toxin A precursor (speA) genes,	
		complete cds.	
ACCESSION	U40453	M19350	
VERSION	U40453.1	GI:1877426	
KEYWORDS		erythrogenic toxin, type A streptococcal exotoxin.	
SOURCE		Streptococcus pyogenes phage T12	
ORGANISM		Streptococcus pyogenes phage T12	
REFERENCE	1	(bases 2782 to 4621)	
AUTHORS		Weeks, C.R. and Ferretti, J.J.	
TITLE		Nucleotide sequence of the type A streptococcal exotoxin	
		(erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage	
		T12	
JOURNAL	Infect. Immun.	52 (1), 144-150 (1986)	
MEDLINE	86166804		
PUBMED	3514452		
REFERENCE	2	(bases 1 to 4621)	
AUTHORS		McShan, W.M., Tang, Y.F. and Ferretti, J.J.	
TITLE		Bacteriophage T12 of Streptococcus pyogenes integrates into the	
		gene encoding a serine tRNA	
JOURNAL	Mol. Microbiol.	23 (4), 719-728 (1997)	
MEDLINE	97206150		
PUBMED	9157243		
REFERENCE	3	(bases 1 to 4621)	

AUTHORS	McShan, W.M., Tang, Y.-F. and Ferretti, J.J.
Direct Submission	
Submitted (09-NOV-1995)	William M. McShan, Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 S. L. Young Blvd., Oklahoma City, OK 73104, USA
COMMENT	On Mar 12, 1997 this sequence version replaced gi:216177.
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4426..4456  
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mat\_peptide

terminator

ORIGIN

Query Match 90.1%; Score 1668.4; DB 7; Length 4621;  
Best Local Similarity 97.4%; Pred. No. 4e-230;  
Matches 1772; Conservative 0; Mismatches 36; Indels 12; Gaps 7;  
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Db GAGTTACCAATCACTTCTATATTTGACAACTAAATGACAACTTCAATATTTTTC 3164  
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RESULT 9  
AE014161  
LOCUS  
DEFINITION Streptococcus pyogenes MGAS315, section 26 of the complete  
genome.  
ACCESSION AE014161 AE014074  
VERSION AE014161.1 GI:21905010  
KEYWORDS

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SOURCE	Streptococcus pyogenes MGAS315	gene	/gene="SpyM3_1272"
ORGANISM	Streptococcus pyogenes MGAS315		/notes="best blastp hit: gb AAL98141.1  (AE010071)
REFERENCE	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		hypothetical protein [Streptococcus pyogenes MGAS8232]"
AUTHORS	Streptococcus.		/codon_start=1
	1 (bases 1 to 57506)		/transl_table=11
	Beres, S.B., Sylva, G.L., Barbican, K.D., Lei, B., Hoff, J.S.,		/product="hypothetical protein"
	Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F.,		/protein_id="AAW79877.1"
	Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and		/db_xref="GI:21905013"
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TITLE	Genome sequence of a serotype M3 strain of group A Streptococcus:		ENKGGAIPLNSKDIILDLFLERPKKSCDFDKLFEAKENKMPKLIYQWGLTF
	Phage-encoded toxins, the high-virulence phenotype, and clone		ALSFAGCEILSDINNDELSKLPKESHLQGLDTSLLSLLPQPFITKYDFEYVK
	emergence		LSVLAQYTSRNKVGSPYTAHSVIEICILYLAKEISLYFESLDNSHLQLEILDYN
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)		DEWPFIDDDMSYTFLYTDIYIEEDSLYHKNWFVQFYL"
REFERENCE	2 (bases 1 to 57506)		complement (4129..6777)
AUTHORS	Beres, S.B., Sylva, G.L., Barbican, K.D., Lei, B., Hoff, J.S.,		/gene="vals"
	Mammarella, N.D., Liu, M.-Y., Smoot, J.C., Porcella, S.F.,		/notes="synonym: SpyM3_1273"
	Parkins, L.D., McCormick, J.K., Leung, D.Y.M., Schlievert, P.M. and		complement (4129..6777)
	Musser, J.M.		/gene="vals"
TITLE	Direct Submission		/notes="best blastp hit: gb AAL98142.1  (AE010071) putative
JOURNAL	Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis,		valine-tRNA ligase [Streptococcus pyogenes MGAS8232]"
	Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,		valine_start=1
	Hamilton, MT 59840, USA		/codon_start=1
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ACCESSION AE009982 AE009949  
VERSION AE009982.1 GI:19747622  
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AUTHORS Smoot,J.C., Barbican,K.D., Van Gompel,J.J., Smoot,L.M.,  
Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,  
Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,  
Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.G. and Musser,J.M.  
Genome sequence and comparative microarray analysis of serotype M18  
group A Streptococcus strains associated with acute rheumatic fever  
outbreaks  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002)  
MEDLINE 21927593  
PUBMED 11917108  
REFERENCE 2 (bases 1 to 11900)  
AUTHORS Smoot,J.C., Barbican,K.D., Van Gompel,J.J., Smoot,L.M.,  
Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,  
Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,  
Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.G. and Musser,J.M.  
Direct Submission  
Submitted (31-JAN-2002) Laboratory of Human Bacterial  
Pathogenesis/Rocky Mountain Laboratories/NIH, 903 S. 4th St.,  
Hamilton, MT 59840, USA  
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Qy 482 ATCTCTCACTTTTTCGTGGTGAACACATAAACAATAATCTTTCCGTTTTTACGCACTAT 541
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Qy 542 CGCTACTGTGTCACTTAAATAATACCCCTTATCAATCGCTCTTTTAAACTCATCTATATA 601
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Db 2290 TATCTATTTATAGTTAGCTATTTTTTCACTGTTAGTATATATGTTGTAATCTGTAATAAC 2231
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Db 1390 GAAATTTTATTCGAATCTTTTATTAAGTAAACCCGCTCAATTTGATGAGCGGTTTGT 1331
Qy 1682 CTTATCTAAGGAGCTTTTACCTCCTAA 1708
Db 1330 CTTATCTAAGGAGCTTTTACCTCCTAA 1304

RESULT 12
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LOCUS Streptococcus pyogenes speA gene for exotoxin type A (scarlet fever toxin).
DEFINITION
ACCESSION X03929.1 GI:47441
VERSION exotoxin; exotoxin type A; speA gene.
KEYWORDS Streptococcus pyogenes
SOURCE Streptococcus pyogenes
ORGANISM Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 1031)
AUTHORS Johnson,L.P.; L'italien,J.J. and Schlievert,P.M.
TITLE Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus enterotoxin B
JOURNAL Mol. Gen. Genet. 203 (2), 354-356 (1986)
MEDLINE 86284313
PUBMED 3526093

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RESULT 13
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LOCUS
DEFINITION
Sequence 993 from Patent WO0123604.
ACCESSION
AX110260
VERSION
AX110260.1 GI:13926552
KEYWORDS
Streptococcus pyogenes
ORGANISM
Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE
1 Bergeron,M.G., Boissinot,M., Huletsky,A., m Hard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL
Patent: WO 0123604-A 993 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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LOCUS
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ACCESSION
X61560
VERSION
X61560.1 GI:47287
KEYWORDS
exotoxin; exotoxin type A.
SOURCE
Streptococcus pyogenes
ORGANISM
Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE
1 Nelson,K., Schlievert,P.M., Sclander,R.K. and Musser,J.M.
AUTHORS
Characterization and clonal distribution of four alleles of the
TITLE
speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
JOURNAL
Streptococcus pyogenes
MEDLINE
J. Exp. Med. 174 (5), 1271-1274 (1991)
92044323
PUBMED
1940804
REFERENCE
2 (bases 1 to 708)
Nelson,K.
AUTHORS
Direct Submission
TITLE
Submitted (01-SEP-1991) K. Nelson, Pennsylvania State University,
JOURNAL
Inst of Mol Evolutionary Genetics, University Park, PA 16802, USA
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Best Local Similarity 99.9%; Pred. No. 5e-92;
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LOCUS S.pyogenes strain MGAS165 speA gene (allele 1) for type A exotoxin.
DEFINITION X61556
ACCESSION X61556
VERSION X61556.1 GI:47291
KEYWORDS exotoxin; exotoxin type A.
SOURCE Streptococcus pyogenes
ORGANISM Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

REFERENCE 1
Nelson,K., Schlievert,P.M., Selander,R.K. and Musser,J.M.
AUTHORS Characterization and clonal distribution of four alleles of the
TITLE speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes
JOURNAL J. Exp. Med. 174 (5), 1271-1274 (1991)
MEDLINE 92044323
PUBMED 1940804
REFERENCE 2 (bases 1 to 708)
Nelson,K.
AUTHORS Direct Submission
TITLE Submitted (01-SEP-1991) K. Nelson, Pennsylvania State University,
JOURNAL Inst of Mol Evolutionary Genetics, University Park, PA 16802, USA
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Best Local Similarity 99.9%; Pred. No. 5e-92;
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Qy 1512 ATGATATATAAGATAATGAAACGTTGACTCAAAACACAGCCAAATT 1559  
Db 661 ATGATATATAAGATAATGAAACGTTGACTCAAAACACAGCCAAATT 708

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GenCore version 5.1.6  
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:.\*  
1: Geneseqn1980s:.\*  
2: Geneseqn1990s:.\*  
3: Geneseqn2000s:.\*  
4: Geneseqn2001as:.\*  
5: Geneseqn2001bs:.\*  
6: Geneseqn2002s:.\*  
7: Geneseqn2003as:.\*  
8: Geneseqn2003bs:.\*  
9: Geneseqn2003cs:.\*  
10: Geneseqn2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1851	100.0	1851	2	AAT51716 Streptoco
2	1851	100.0	1851	2	AAV41593 Nucleotid
3	1835.4	99.2	1837	2	AAT28540 S. pyogen
4	1835.4	99.2	1837	4	ABA76857 Streptoco
5	1832.2	99.0	1837	3	AAZ51112 Streptoco
6	1832.2	99.0	1837	6	ABN84229 Streptoco
7	1832.2	99.0	1837	7	ACA61184 DNA encod
8	1832.2	99.0	1837	8	AAD56771 Streptoco
9	1830.6	98.9	1837	8	ACD28901 Streptoco
10	832.8	48.2	1031	7	ACA64700 S. pyogen
11	754.4	40.8	756	4	AAH01002 Unidentif
12	656.8	35.5	1419	8	ACD28908 SPEA L42R
13	656.8	35.5	1419	8	AAD56778 Streptoco
14	278	15.0	1497	7	ACA64721 Streptoco
15	184.2	10.0	1712	3	AAZ51107 Staphyloc
16	184.2	10.0	1712	6	ABN84224 Staphyloc
17	184.2	10.0	1712	7	ACA61179 DNA encod
18	184.2	10.0	1712	8	ACA64695 S. aureus
19	184.2	10.0	1712	8	ACD28896 S. aureus
20	184.2	10.0	1712	8	AAD56766 DNA #3 re
21	178.8	9.7	110000	6	Continuation (6 of
22	176.2	9.5	1712	3	AAZ51108 Mutant St
23	176.2	9.5	1712	6	ABN84225 Staphyloc

24	176.2	9.5	1712	7	ACA61180	ACA61180 DNA encod
25	176.2	9.5	1712	8	ACD28897	ACD28897 S. aureus
26	176.2	9.5	1712	8	AAD56767	AAD56767 DNA #4 re
27	171.4	9.3	773	2	AAT45698	AAT45698 Staphyloc
28	171	9.2	886	7	ACA64689	ACA64689 S. aureus
29	169.2	9.1	801	7	ACA64688	ACA64688 S. aureus
30	167.8	9.1	1095	7	ACA64696	ACA64696 S. aureus
31	164.6	8.9	1095	3	AAZ51111	AAZ51111 Staphyloc
32	164.6	8.9	1095	6	ABN84228	ABN84228 Staphyloc
33	164.6	8.9	1095	7	ACA61183	ACA61183 DNA encod
34	164.6	8.9	1095	8	ACD28900	ACD28900 S. aureus
35	164.6	8.9	1095	8	AAD56770	AAD56770 Staphyloc
36	161.2	8.7	723	3	AAZ45835	AAZ45835 Mutant SE
37	161.2	8.7	801	3	AAZ45834	AAZ45834 Mutant SE
38	161.2	8.7	1388	3	AAZ51109	AAZ51109 Mutant St
39	161.2	8.7	1388	6	ABN84226	ABN84226 Staphyloc
40	161.2	8.7	1388	7	ACA61181	ACA61181 DNA encod
41	161.2	8.7	1388	8	ACD28898	ACD28898 S. aureus
42	161.2	8.7	1388	8	AAD56768	AAD56768 DNA #5 re
43	159.6	8.6	867	4	AAH74983	AAH74983 Nucleotid
44	145.8	7.9	177	6	ABN66731	ABN66731 Streptoco
45	130.6	7.1	186	6	ABN66706	ABN66706 Streptoco

ALIGNMENTS

RESULT 1  
AAT51716  
ID AAT51716 standard; DNA; 1851 BP.

AC AAT51716;

DT 04-NOV-1997 (first entry)

DE Streptococcus pyogenes Streptococcal toxin A DNA.

Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;  
protection; treatment; cancer; neutralising antibody;  
Streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;  
hypotension; group A streptococcal infection; myositis; fasciitis;  
liver damage; T cell; lymphoma; ovarian; uterine; ss.

OS Streptococcus pyogenes.

EH Key Location/Qualifiers

FT CDS 828..1583

FT sig\_peptide /\*tag= a

FT mat\_peptide /\*tag= b

FT /\*tag= c

FT /product= "Streptococcal\_toxin\_A"

WO9640930-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US010252.

07-JUN-1995; 95US-00480261.

(MINU ) UNIV MINNESOTA.

Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

WPI; 1997-099936/09.

P-PSDB; AAW12097.

Mutant SPE-A toxin with at least one amino acid change is substantially

non-lethal - used in vaccine composition for treatment of cancer and

streptococcal toxic shock syndrome etc.

Handwritten signature and date: 10/10/04

PS Disclosure; Page 77-79; 102pp; English.

XX The present sequence encodes Streptococcus pyogenes Streptococcal toxin A (SPE-A), from which a non-lethal mutant SPE-A, comprising at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fasciitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells

XX

SQ Sequence 1851 BP; 635 A; 326 C; 248 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 1851; DB 2; Length 1851;

Best Local Similarity 100.0%; Pred. No. 4.5e-289;

Matches 1851; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCAGCATCACTCATGTTTGACAGCTTATCATCGATAGCTTACCTTTGCAATCAGG 60

DB 1 CCATCAGCATCACTCATGTTTGACAGCTTATCATCGATAGCTTACCTTTGCAATCAGG 60

QY 61 TCTATCCTTGAACAGGTGCAACATAGATTAGGCGATGAGATTTACCAGACCACTATGA 120

DB 61 TCTATCCTTGAACAGGTGCAACATAGATTAGGCGATGAGATTTACCAGACCACTATGA 120

QY 121 AGGTATATCTCACTACGCAATGGCAATTGATGACATTTGGAATCAATCAAT 180

DB 121 AGGTATATCTCACTACGCAATGGCAATTGATGACATTTGGAATCAATCAAT 180

QY 181 TTGTTACTAACAGCACTAGATTGCACTAATTTCTCAACAAAGTTTAAATTTAAACA 240

DB 181 TTGTTACTAACAGCACTAGATTGCACTAATTTCTCAACAAAGTTTAAATTTAAACA 240

QY 241 TTCAAGTAACTCCACAGCTCCATCAATGCTTACCGTAAAGTAAATCAATCAATCA 300

DB 241 TTCAAGTAACTCCACAGCTCCATCAATGCTTACCGTAAAGTAAATCAATCAATCA 300

QY 301 CTTGTTTACATCAAGTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 360

DB 301 CTTGTTTACATCAAGTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 360

QY 361 TTATTGACAACTAAATTTGACAACTTTCAATTTTCTTTTCTTTTCTTTTCTTTTCT 420

DB 361 TTATTGACAACTAAATTTGACAACTTTCAATTTTCTTTTCTTTTCTTTTCTTTTCT 420

QY 421 ATTGATATAGTCTAATTCACATCTTCCACTCTCTCTCTCTCTCTCTCTCTCTCT 480

DB 421 ATTGATATAGTCTAATTCACATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480

QY 481 CATCTCTCACTTTTCTGTTGGTAAACACATATCAATATCTTTCCGTTTTTACGCAC 540

DB 481 CATCTCTCACTTTTCTGTTGGTAAACACATATCAATATCTTTCCGTTTTTACGCAC 540

QY 541 TCCTCTACTGTGTCCTAAATATATACCCCTTATCAATCGCTTTTAACTCATCTAT 600

DB 541 TCCTCTACTGTGTCCTAAATATATACCCCTTATCAATCGCTTTTAACTCATCTAT 600

QY 601 ATAACTATTTTCT 660

DB 601 ATAACTATTTTCT 660

QY 661 TTTTGTATTTTATATAAATTTATTAATAGTTAAATTTTAAATTTTAAATTTTAA 720

DB 661 TTTTGTATTTTATATAAATTTATTAATAGTTAAATTTTAAATTTTAAATTTTAA 720

QY 721 TTATTCTATTTATAGTTAGCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780

DB 721 TTATTCTATTTATAGTTAGCTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780

QY 781 CTTTAAATCTAGAGGAAACCCAGATATAAATGGAGGATATTAATGGAACCAATA 840

DB 781 CTTTAAATCTAGAGGAAACCCAGATATAAATGGAGGATATTAATGGAACCAATA 840

QY 841 AAAAAGTATTGAAGAAAATGGTATTTTGTGTTTGTAGTGACATTTCTTGGACTTAA 900

DB 841 AAAAAGTATTGAAGAAAATGGTATTTTGTGTTTGTAGTGACATTTCTTGGACTTAA 900

QY 901 CGAAGAGGTATTGCTCAACAGACCCCGATCCAGCCAACTTCCACAGATCTAGTTT 960

DB 901 CGAAGAGGTATTGCTCAACAGACCCCGATCCAGCCAACTTCCACAGATCTAGTTT 960

QY 961 TTAATAACCTTCAAAATATATATTTCTTTATGAGGTTGACCTGTTTACTCAGGAATG 1020

DB 961 TTAATAACCTTCAAAATATATATTTCTTTATGAGGTTGACCTGTTTACTCAGGAATG 1020

QY 1021 TGAATCTGTTGATCAACTTTTATCTCACCATTTAATATATATATGTTTCAGGCCAAAT 1080

DB 1021 TGAATCTGTTGATCAACTTTTATCTCACCATTTAATATATATATGTTTCAGGCCAAAT 1080

QY 1081 ATGATAAATTAATAAATCTGAACCTTAAGAACCAAGAGATGGCACTTTTATTAAGGATA 1140

DB 1081 ATGATAAATTAATAAATCTGAACCTTAAGAACCAAGAGATGGCACTTTTATTAAGGATA 1140

QY 1141 ACCTTGATTTTATGTTGATAGATATTAATCTCTCTGTTTATTTATGTTGAAAATG 1200

DB 1141 ACCTTGATTTTATGTTGATAGATATTAATCTCTCTGTTTATTTATGTTGAAAATG 1200

QY 1201 GAGTGCATCTATCTACGAGGGGTAAACAAATCATCAAGGGATCATTTTGAATAATTCCT 1260

DB 1201 GAGTGCATCTATCTACGAGGGGTAAACAAATCATCAAGGGATCATTTTGAATAATTCCT 1260

QY 1261 AAAAGATAGTCGTTAAAGTATCAATCGATGTTATCAATCGATGTTATCAATCGATGTT 1320

DB 1261 AAAAGATAGTCGTTAAAGTATCAATCGATGTTATCAATCGATGTTATCAATCGATGTT 1320

QY 1321 CAATAAATAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1380

DB 1321 CAATAAATAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1380

QY 1381 ATATAAGCAACTATATATCTTAATGAGCTTCTTAATGAGCTTCTTAATGAGCTTCTTA 1440

DB 1381 ATATAAGCAACTATATATCTTAATGAGCTTCTTAATGAGCTTCTTAATGAGCTTCTTA 1440

QY 1441 TACCTAAGATAAAGAAAGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1500

DB 1441 TACCTAAGATAAAGAAAGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1500

QY 1501 CTAAATCTTATGATATATAAAGATTAATGAAACGCTTGAACCTTGAACCTTGAACCTTGA 1560

DB 1501 CTAAATCTTATGATATATAAAGATTAATGAAACGCTTGAACCTTGAACCTTGAACCTTGA 1560

QY 1561 AAGTCTACCTAACAACCAAGTAACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1620

DB 1561 AAGTCTACCTAACAACCAAGTAACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1620

QY 1621 AGAAATTTTATGCAATTTCTTTTATTAATGTAAGTAAACCGCTCAATTTGATGAGCGTT 1680

DB 1621 AGAAATTTTATGCAATTTCTTTTATTAATGTAAGTAAACCGCTCAATTTGATGAGCGTT 1680

QY 1681 TCTTATCTAAGGAGCTTTTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740

DB 1681 TCTTATCTAAGGAGCTTTTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740

QY 1741 TTTCTCTATTTGTTATTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1800

DB 1741 TTTCTCTATTTGTTATTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1800

QY 1801 AACCAAAATCATAGACAGGCTTGTAGCTTAGCAACTATTTTATCGTC 1851

DB 1801 AACCAAAATCATAGACAGGCTTGTAGCTTAGCAACTATTTTATCGTC 1851



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QY	181	TTGTTACTAA	CGAGCACTAG	ATTGACCAACTAAT	TCTC	CAACAAACGTTAA	TTTAAACAACA	240
DB	181	TTGTTACTAA	CGAGCACTAG	ATTGACCAACTAAT	TCTC	CAACAAACGTTAA	TTTAAACAACA	240
QY	241	TTCAAGTAACT	CCCCAGCAGCT	CCATCAAT	CGCTTAC	CGTAAAGTAAT	CATAACTTAC	300
DB	241	TTCAAGTAACT	CCCCAGCAGCT	CCATCAAT	CGCTTAC	CGTAAAGTAAT	CATAACTTAC	300
QY	301	CCCTGTTACAT	CAAGAGTTT	TTTCTTTT	TGCTTGT	CTTGTAC	GATTACATAA	360
DB	301	CCCTGTTACAT	CAAGAGTTT	TTTCTTTT	TGCTTGT	CTTGTAC	GATTACATAA	360
QY	361	TTATTCACAACT	AAATGACAACT	CTCTTCAAT	TATTTT	CTGTCTACT	CAAAAGTTTCTTC	420
DB	361	TTATTCACAACT	AAATGACAACT	CTCTTCAAT	TATTTT	CTGTCTACT	CAAAAGTTTCTTC	420
QY	421	ATTTGTATAGT	CTAATTTCC	ACCATCACT	TCTTCCACT	CTCTAC	CGTCAACA	480
DB	421	ATTTGTATAGT	CTAATTTCC	ACCATCACT	TCTTCCACT	CTCTAC	CGTCAACA	480
QY	481	CATCTCTCACT	TTTTCGTGTGGT	AAACATAAT	CAAAATAT	CTTTCCGTT	TTTTTACGCACTA	540
DB	481	CATCTCTCACT	TTTTCGTGTGGT	AAACATAAT	CAAAATAT	CTTTCCGTT	TTTTTACGCACTA	540
QY	541	TCGCTACTGTG	CACCTAAATAT	TACCCCTTAT	CAATCGCTT	CTTTAAAC	CTCATCTATAT	600
DB	541	TCGCTACTGTG	CACCTAAATAT	TACCCCTTAT	CAATCGCTT	CTTTAAAC	CTCATCTATAT	600
QY	601	ATAACATATTT	CACTCTACCTA	CTCTATCGT	ATAAAGAT	AAAAAT	ACTATTTGTTT	660
DB	601	ATAACATATTT	CACTCTACCTA	CTCTATCGT	ATAAAGAT	AAAAAT	ACTATTTGTTT	660
QY	661	TTTTGTTATTT	TATATAAAT	TATTAAT	ATAAGTTAA	TGTTTTT	AAAAAATATACAAAT	720
DB	661	TTTTGTTATTT	TATATAAAT	TATTAAT	ATAAGTTAA	TGTTTTT	AAAAAATATACAAAT	720
QY	721	TTATCTCATTT	ATAGTTAGCTA	TTTTTTCA	TGTTAGT	TATATTTGGT	GAAATGTTAA	780
DB	721	TTATCTCATTT	ATAGTTAGCTA	TTTTTTCA	TGTTAGT	TATATTTGGT	GAAATGTTAA	780
QY	781	CTTTTTAAAT	CTAGAGGAGAC	CCAGATATAA	AAATGAGGAAT	TATTAAT	TGAAAAACAATA	840
DB	781	CTTTTTAAAT	CTAGAGGAGAC	CCAGATATAA	AAATGAGGAAT	TATTAAT	TGAAAAACAATA	840
QY	841	AAAAAGTATT	GAGAAAAAT	GGTATTTTT	GTGTTAGTG	ACATTTCT	TGGAATACAATCT	900
DB	841	AAAAAGTATT	GAGAAAAAT	GGTATTTTT	GTGTTAGTG	ACATTTCT	TGGAATACAATCT	900
QY	901	CGCAAGAGTAT	TTTGCTCA	ACAGACCCCGAT	CCAAGCC	ACTTTCACAGAT	CTAGTTAG	960
DB	901	CGCAAGAGTAT	TTTGCTCA	ACAGACCCCGAT	CCAAGCC	ACTTTCACAGAT	CTAGTTAG	960
QY	961	TTAAAAAC	CTTCAAAATAT	TATTTTT	CTTTATG	AGGGTGAC	CCCTGTTACT	1020
DB	961	TTAAAAAC	CTTCAAAATAT	TATTTTT	CTTTATG	AGGGTGAC	CCCTGTTACT	1020
QY	1021	TGAAATCTG	TGATCAACT	TTTTTAT	CTACCAAT	TATTAAT	TAATGTTT	1080
DB	1021	TGAAATCTG	TGATCAACT	TTTTTAT	CTACCAAT	TATTAAT	TAATGTTT	1080
QY	1081	ATGATAAAT	TTAAAAACT	GAACCTTA	AGAACCA	AGAGATG	CGCAACTTTAT	1140
DB	1081	ATGATAAAT	TTAAAAACT	GAACCTTA	AGAACCA	AGAGATG	CGCAACTTTAT	1140
QY	1141	ACGTTGAT	TATTTAT	TGGTGAGAA	TATTAAC	CAATCTCTG	TTTATG	1200
DB	1141	ACGTTGAT	TATTTAT	TGGTGAGAA	TATTAAC	CAATCTCTG	TTTATG	1200
QY	1201	GGAGTGCA	TGTATCT	CTACGGGGG	GTAAACAAAT	CTATGA	AGGGAATCAT	1260
DB	1201	GGAGTGCA	TGTATCT	CTACGGGGG	GTAAACAAAT	CTATGA	AGGGAATCAT	1260
QY	1261	AAAAAGAT	AGTCTG	TTAAAGTAT	CAATCGAT	GTATCCAAAG	CGCTATCA	1320
DB	1261	AAAAAGAT	AGTCTG	TTAAAGTAT	CAATCGAT	GTATCCAAAG	CGCTATCA	1320



QY 555 CCTAAATATACCCCTTATCAATCGCTTCTTTAACTCATCTATATATAACATATTTTCAT 614  
Db 541 CCTAAATATACCCCTTATCAATCGCTTCTTTAACTCATCTATATATAACATATTTTCAT 600  
QY 615 CTTCTACCTATCTATTCGTAAGAAAGATAAATAAATACTATGTTTTTTTGTATTTTAT 674  
Db 601 CTTCTACCTATCTATTCGTAAGAAAGATAAATAAATACTATGTTTTTTTGTATTTTAT 660  
QY 675 AATAAATATTAATTAATTAAGTAAATGTTTTTTTAAATAATACAAATTTTCTATTATTA 734  
Db 661 AATAAATATTAATTAATTAAGTAAATGTTTTTTTAAATAATACAAATTTTCTATTATTA 720  
QY 735 GTTAGCTATTTTTCATTTGTTAGTAAATGTTGTAATGTAAPACCTTTTAAATCTAG 794  
Db 721 GTTAGCTATTTTTCATTTGTTAGTAAATGTTGTAATGTAAPACCTTTTAAATCTAG 780  
QY 795 AGGAGAACCCAGATATAAATGAGGAAATTAATGGAACAATTAATAAAGATATTGAAG 854  
Db 781 AGGAGAACCCAGATATAAATGAGGAAATTAATGGAACAATTAATAAAGATATTGAAG 840  
QY 855 AAAATGTAATTTTGTGTTAGTGAATTTCTTGGACTAACTCTCGCAAGAGTATT 914  
Db 841 AAAATGTAATTTTGTGTTAGTGAATTTCTTGGACTAACTCTCGCAAGAGTATT 900  
QY 915 GCTCAACAGACCCCGATCCAGCAACTTTCAGAGATCTAGTTAGTTAAACCTTCAA 974  
Db 901 GCTCAACAGACCCCGATCCAGCAACTTTCAGAGATCTAGTTAGTTAAACCTTCAA 960  
QY 975 AATATATATTTTCTTTATGAGGCTGACCCCTGTTACTCACGAGATGTGAATCTGTTGAT 1034  
Db 961 AATATATATTTTCTTTATGAGGCTGACCCCTGTTACTCACGAGATGTGAATCTGTTGAT 1020  
QY 1035 CAACCTTTTATCTCAACCAATTAATATATATATGTTTTCAGGGCCAAATATGATTAATAA 1094  
Db 1021 CAACCTTTTATCTCAACCAATTAATATATATATGTTTTCAGGGCCAAATATGATTAATAA 1080  
QY 1095 ACTGAACCTTAAGACCAAGAGATGGCACTTTTAAAGGATATAAAGCTGTTGATTTAT 1154  
Db 1081 ACTGAACCTTAAGACCAAGAGATGGCACTTTTAAAGGATATAAAGCTGTTGATTTAT 1140  
QY 1155 GGTGTAGAAATATACCATCTCTGTTATTTAATGTAAGAAATCGAAGAGGTGATGATC 1214  
Db 1141 GGTGTAGAAATATACCATCTCTGTTATTTAATGTAAGAAATCGAAGAGGTGATGATC 1200  
QY 1215 TAGGAGGGGTACAAATCATGAGGGAATCAATTAAGAAATCTTAAAGATAGTCGTT 1274  
Db 1201 TAGGAGGGGTACAAATCATGAGGGAATCAATTAAGAAATCTTAAAGATAGTCGTT 1260  
QY 1275 AAAGTATCAATCGATGCTATCCAAAGCCTATCTATTTGATATTTGAAACAAATAAAAAATG 1334  
Db 1261 AAAGTATCAATCGATGCTATCCAAAGCCTATCTATTTGATATTTGAAACAAATAAAAAATG 1320  
QY 1335 GTAACTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATATAAGCAACTA 1394  
Db 1321 GTAACTGCTCAAGAAATAGACTATAAAGTTAGAAATATCTTACAGATATAAGCAACTA 1380  
QY 1395 TATACTAATGACCTCTTAAATGAACTGGATATATAAAGTTACATACCTTAAGATAAA 1454  
Db 1381 TATACTAATGACCTCTTAAATGAACTGGATATATAAAGTTACATACCTTAAGATAAA 1440  
QY 1455 GAAAGTTTTGGTTGATTTTTTCCCTGAAACCAAGATTTCTCAATCTAAATATCTTATG 1514  
Db 1441 GAAAGTTTTGGTTGATTTTTTCCCTGAAACCAAGATTTCTCAATCTAAATATCTTATG 1500  
QY 1515 ATATATAAGATATGAACCGTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCA 1574  
Db 1501 ATATATAAGATATGAACCGTTGACTCAACACAGCCAAATTTGAAGTCTACCTAACCA 1560  
QY 1575 ACCAAGTAACCTTTTGTCTTTTGGCAACCTTACCTACTGCTGGATTTTGAATTTTATGTC 1634  
Db 1561 ACCAAGTAACCTTTTGTCTTTTGGCAACCTTACCTACTGCTGGATTTTGAATTTTATGTC 1620

QY 1635 AATCTTTTATTAATGTAAACACCGCTCATTTGATGAGCGGTTTTGTTCTTATCTAAAGGA 1694  
Db 1621 AATCTTTTATTAATGTAAACACCGCTCATTTGATGAGCGGTTTTGTTCTTATCTAAAGGA 1680  
QY 1695 GCTTTACTCTTAATGCTGCAAAATTTTAAATGTTGATTTTGTATTTGTTCTATTCTAT 1754  
Db 1681 GCTTTACTCTTAATGCTGCAAAATTTTAAATGTTGATTTTGTATTTGTTCTATTCTAT 1740  
QY 1755 TTGATGGGTAATCCCATTTTTCGACAGACATCGTCGTCGCCACCTCTTAACACCAAAATCAT 1814  
Db 1741 TTGATGGGTAATCCCATTTTTCGACAGACATCGTCGTCGCCACCTCTTAACACCAAAATCAT 1800  
QY 1815 AGACAGGAGCTGTAGCTTAGCACTATTTATCGTC 1851  
Db 1801 AGACAGGAGCTGTAGCTTAGCACTATTTATCGTC 1837

## RESULT 4

ABA76857  
ID ABA76857 standard; DNA; 1837 BP.

XX AC ABA76857;

XX XX 28-JAN-2002 (first entry)

XX Streptococcus pyogenes polynucleotide SEQ ID NO 33.

XX DE Detection; bacterial species; animal; food; environment;  
XX KW antibiotic resistance; ds.

XX OS Streptococcus pyogenes.

XX PN NZ501596-A.

XX PD 29-JUN-2004

XX PF 12-SEP-1995; 95NZ-00501596.

XX PR 12-SEP-1995; 95NZ-00501596.

XX PA (IDI-) IDI INFECTION DIAGNOSTIC INC.

XX PI Bergeron MG, Ouellette M, Roy PH;

XX DR WPI; 2001-615034/71.

XX PT Method for detecting target bacterial species in a sample, comprises  
XX PT detecting the presence or amount of bacterial nucleic acid amplified by a  
XX PT primer derived from bacterial DNA, specific for the target bacterial  
XX PT species.

XX PS Claim 6; Page 107-108; 168pp; English.

XX CC The invention relates to detecting target bacterial species suspected to  
XX CC be present in a sample, comprising contacting nucleic acids of target  
XX CC bacterial species with an amplification primer pair derived from a  
XX CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target  
XX CC bacterial species but ubiquitous for different strains, amplifying the  
XX CC nucleic acid and detecting the presence or amount of an amplified  
XX CC sequence as an indication of the presence or amount of the target  
XX CC bacterial species. The invention includes primers and probes (ABA76862-  
XX CC ABA76984) against the target bacterial species, especially E.coli,  
XX CC K.pneumoniae, P.aeruginosa, P.mirabilis, S.pneumoniae, S.aureus,  
XX CC S.epidermidis, E.faecalis, S.saprophyticus, S.pyogenes, H.influenzae,  
XX CC M.cattarrhalis and/or group A streptococci producing exotoxin A gene spe  
XX CC A, suspected to be present in a sample which is obtained from human  
XX CC patients, animals, environment or food, and which consists of one or more  
XX CC bacterial colonies. Oligonucleotide probes and primers complementary to  
XX CC the bacterial genes encoding resistance to antibiotics such as bla(tem),  
XX CC bla(xba), bla(shv), aadB, aacC1, aacC2, aacC3, aacC4, mecA, vanA, vanH,  
XX CC vanX, satA, aacA-aphD, vat, vga, msrA, sul and/or int (ABA76985-ABA77001)  
XX CC are also useful to identify commonly encountered and clinically important  
XX CC resistance genes. The invention provides a rapid method of bacterial

*Handwritten signature*

CC identification that can be achieved, which reduces the time currently  
CC required for the identification of pathogens in the clinical laboratory  
XX  
SQ Sequence 1837 BP; 631 A; 318 C; 248 G; 640 T; 0 U; 0 Other;

Query Match	99.2%	Score 1835.4;	DB 4;	Length 1837;
Best Local Similarity	99.9%	Pred. No. 1.4e-286;		
Matches 1836; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	15	TCATGTTTGCAGCCTTATATCGATAGACTTACTATCTTTTCGAATCAGGTCCTATCCTTTGAAC	74
Db	1	TCATGTTTGCAGCCTTATATCGATAGACTTACTATCTTTTCGAATCAGGTCCTATCCTTTGAAC	60
Qy	75	AGGTGCAACATATAGATTAGGCGATCGAGATTTACGAGCAACTATGAACTGATATACTCAC	134
Db	61	AGGTGCAACATATAGATTAGGCGATCGAGATTTACGAGCAACTATGAACTGATATACTCAC	120
Qy	135	ATCAGCGAATCGGCAATTGATGACATTTGGAACTAAATCAATCAATTTGTTACTTAACAAG	194
Db	121	ATCAGCGAATCGGCAATTGATGACATTTGGAACTAAATCAATCAATTTGTTACTTAACAAG	180
Qy	195	CAACTAGATTGACAACTAAATCTCAACAAAAGTAAATTAACAACATTTCAAGTAAGTACCC	254
Db	181	CAACTAGATTGACAACTAAATCTCAACAAAAGTAAATTAACAACATTTCAAGTAAGTACCC	240
Qy	255	ACGAGCTCCATCAATGCTTACCGTAAGTAATCATAACTTACTAAACCTGTTGATCAACA	314
Db	241	ACGAGCTCCATCAATGCTTACCGTAAGTAATCATAACTTACTAAACCTGTTGATCAACA	300
Qy	315	GGTTTTTCTTTTTCTTTTTCTTTGTTTCATGAGTTACCACTAACTTCTATATTTATTGACAACATA	374
Db	301	GGTTTTTCTTTTTCTTTTTCTTTGTTTCATGAGTTACCACTTCTATATTTATTGACAACATA	360
Qy	375	ATTGACAACTCTTCAAAATATTTTTCTGTCTACTCAAAGTTTTCTTCATTTGATAPAGCT	434
Db	361	ATTGACAACTCTTCAAAATATTTTTCTGTCTACTCAAAGTTTTCTTCATTTGATAPAGCT	420
Qy	435	AATTTCCACCATCACTTCTTCCACTCTCTACTACCGTCAACAATTCATCATCTCTCACTTTT	494
Db	421	AATTTCCACCATCACTTCTTCCACTCTCTACTACCGTCAACAATTCATCATCTCTCACTTTT	480
Qy	495	TCGTGTGTGTAACACATAATACTAAATATCTTCCGTTTTTTACGCACATCTCGCTACTGTGCA	554
Db	481	TCGTGTGTGTAACACATAATACTAAATATCTTCCGTTTTTTACGCACATCTCGCTACTGTGCA	540
Qy	555	CCTAAAAATATACCCCTTATCAATCGTTCTTTTAAACTCATCTATATATAACATATTTTAT	614
Db	541	CCTAAAAATATACCCCTTATCAATCGTTCTTTTAAACTCATCTATATATAACATATTTTAT	600
Qy	615	CCTCCTACTATCTATTCGTAAAAAGATAAAAATAAATTAATTTGTTTTTTTGTATTTTAT	674
Db	601	CCTCCTACTATCTATTCGTAAAAAGATAAAAATAAATTAATTTGTTTTTTTGTATTTTAT	660
Qy	675	AATAAAATATTAATATAAGTTAATGTTTTTTTAAAAATATAACAATTTTATCTTATTTATA	734
Db	661	AATAAAATATTAATATAAGTTAATGTTTTTTTAAAAATATAACAATTTTATCTTATTTATA	720
Qy	735	GTTAGCTATTTTTTTCATTTGTTAGTAATAATGTTGGAATTTGTAATAACCTTTTTTAAATCTAG	794
Db	721	GTTAGCTATTTTTTTCATTTGTTAGTAATAATGTTGGAATTTGTAATAACCTTTTTTAAATCTAG	780
Qy	795	AGGAGAACCCAGATATAAAATGGAGGAATTAATTAATGGAAAAACAATAAAAAAGTATTTGAAG	854
Db	781	AGGAGAACCCAGATATAAAATGGAGGAATTAATTAATGGAAAAACAATAAAAAAGTATTTGAAG	840
Qy	855	AAAAATGGTATTTTTTGTTTTGTAGTGACATTTCTTGGACTTAAACAATCTCGCAAGAGGTATTT	914
Db	841	AAAAATGGTATTTTTTGTTTTGTAGTGACATTTCTTGGACTTAAACAATCTCGCAAGAGGTATTT	900
Qy	915	GCTCAACGAAGCCCCGATCCAAAGCCAACTTCAAGATCTAGTTTATGTTTAAAAAACCCTTCAA	974
Db	901	GCTCAACGAAGCCCCGATCCAAAGCCAACTTCAAGATCTAGTTTATGTTTAAAAAACCCTTCAA	960

RESULT 5
AAZ51112
ID AAZ
XX
AC AAZ
XX
DT 05 -
XX
DE Str
XX
KW Sup
KW ant

XX Streptococcal pyrogenic exotoxin A (SPE-A) encoding DNA.

XX Superantigen toxin; SAG; Streptococcal pyrogenic exotoxin A; SPE-A;  
KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;  
KW

KW cytotatic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA42;  
XW diagnosis; treatment; superantigen-associated bacterial infection; ds.  
XX

OS Streptococcus sp.

XX Key Location/Qualifiers  
FH CDS 814..1569  
PT /tag= a  
FT /product= "Streptococcal pyrogenic exotoxin A (SPE-A)"  
XX

XX W0200009154-A1.

XX 24-FEB-2000.

XX 13-AUG-1998; 98WO-US016766.

XX 13-AUG-1998; 98WO-US016766.

XX (SEED-) REED ARMY INST RES WALTER.

XX Ulrich RG, Olson MA, Bavari S;

XX WPI; 2000-224177/19.

XX P-PSDB; AAY70109.

XX Nucleic acid encoding superantigen toxin useful as a vaccine and for  
PT diagnosis of superantigen-associated bacterial infections.

XX Example 12; Page 92-94; 118pp; English.

XX The present sequence is the DNA encoding Streptococcal pyrogenic exotoxin  
CC A (SPE-A), a bacterial superantigen toxin (Sag), used for the formulation  
CC of SPE-A vaccine SPEA42. The coding region of this Sag toxin is altered  
CC by site directed mutagenesis, introducing L42R mutation, that results in  
CC disruption of binding of the toxin to both the MHC class II or T-cell  
CC antigen receptor. SPE-A has antibacterial and cytostatic activity. This  
CC sequence is useful for the production of SPE-A vaccines and specific  
CC antibodies. This vaccine overcomes the disadvantages of the chemically  
CC inactivated toxoids and is designed to protect individuals against one or  
CC several related staphylococcal and streptococcal toxins. It is used for  
CC the diagnosis and treatment or amelioration of superantigen-associated  
CC bacterial infections

XX Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

XX Query Match 99.0%; Score 1832.2; DB 3; Length 1837;

XX Best Local Similarity 99.8%; Pred. No. 4.7e-286;

XX Matches 1834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 TCATGTTTGACAGCTTATCATGATAAGCTTACTTTTCGAATCAGGCTCTATCCTCGAAC 74

DB 1 TCATGTTTGACAGCTTATCATGATAAGCTTACTTTTCGAATCAGGCTCTATCCTCGAAC 60

QY 75 AGGTGCAACATAGATTAGGCGATGGAGATTACAGACAACTATGAACGATATATCTAC 134

DB 61 AGGTGCAACATAGATTAGGCGATGGAGATTACAGACAACTATGAACGATATATCTAC 120

QY 135 ATCCGCAATCGCAATGATGACATTTGGAATCAATTAATTCATCAATTTGTTTACTTAA 194

DB 121 ATCCGCAATCGCAATGATGACATTTGGAATCAATTAATTCATCAATTTGTTTACTTAA 180

QY 195 CAACATAGATTGACAACTAATTTCTCAACAAAGGTTTAAATTTAACCAATTCAGTAACCTCC 254

DB 181 CAACATAGATTGACAACTAATTTCTCAACAAAGGTTTAAATTTAACCAATTCAGTAACCTCC 240

QY 255 ACCAGTCCCATGATGCTACCGTAAGTAATCATCACTTACTTAAACCTTTGTTTACTACAA 314

DB 241 ACCAGTCCCATGATGCTACCGTAAGTAATCATCACTTACTTAAACCTTTGTTTACTACAA 300

QY 315 GGTGTTTCTTTTGTCTGTTGATGAGTACCATAACTTTCTATATATTATTTGACAACTAA 374

DB 301 GGTGTTTCTTTTGTCTGTTGATGAGTACCATAACTTTCTATATATTATTTGACAACTAA 360

QY 375 ATTGCAACTCTTCAATTAATTTTCTGCTACTCAAAAGTTTTCCTTCTATTGATAGTCT 434  
DB 361 ATTGCAACTCTTCAATTAATTTTCTGCTACTCAAAAGTTTTCCTTCTATTGATAGTCT 420  
QY 435 AATTCACCATCATCTTCTTCCACTCTCTTACCGTCAACACTTCATCTCTCCTCCTTTT 494  
DB 421 AATTCACCATCATCTTCTTCCACTCTCTTACCGTCAACACTTCATCTCTCCTCCTTTT 480  
QY 495 TCGTGTGTGTAACACATAATCAATTAATTTTCTGCTACTCAAAAGTTTTCCTTCTATTG 554  
DB 481 TCGTGTGTGTAACACATAATCAATTAATTTTCTGCTACTCAAAAGTTTTCCTTCTATTG 540  
QY 555 CCTAAATATATACCCCTTATCAATCGCTTCTTTAAACATCATCTATATATAATATTTTAT 614  
DB 541 CCTAAATATATACCCCTTATCAATCGCTTCTTTAAACATCATCTATATATAATATTTTAT 600  
QY 615 CCTCTACCTATCTATTCGTAAGAAAGATAAAATAAATTAATTTGTTTCTTTTCTTTTAT 674  
DB 601 CCTCTACCTATCTATTCGTAAGAAAGATAAAATAAATTAATTTGTTTCTTTTCTTTTAT 660  
QY 675 AATRAAATTAATTAATAAGTTAATGTTTAAAAATATACAAATTTTATTTTATTTATA 734  
DB 661 AATRAAATTAATTAATAAGTTAATGTTTAAAAATATACAAATTTTATTTTATTTATA 720  
QY 735 GTTACCTATTTTTCATTTAGTAATTTGCTGAATTTGTAATTAACCTTTTAAATCTAG 794  
DB 721 GTTACCTATTTTTCATTTAGTAATTTGCTGAATTTGTAATTAACCTTTTAAATCTAG 780  
QY 795 AGGAGAACCCAGATATAAAATGAGGAATATTAATGGAACCAATTAATAAAGTATTGAAG 854  
DB 781 AGGAGAACCCAGATATAAAATGAGGAATATTAATGGAACCAATTAATAAAGTATTGAAG 840  
QY 855 AAATGGTATTTTGTGTTTGTAGTGACATTTCTTGACATAACAACTCCCAAGAGTATT 914  
DB 841 AAATGGTATTTTGTGTTTGTAGTGACATTTCTTGACATAACAACTCCCAAGAGTATT 900  
QY 915 GCTCAACAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTGTAGTTAAAAACCTTCAA 974  
DB 901 GCTCAACAGACCCCGATCCCAAGCCAACTTCACAGATCTAGTTTGTAGTTAAAAACCTTCAA 960  
QY 975 AATATATATTTTCTTTTATGAGGGTGACCCGTGTTACTACGAGAAATGTAATCTGTTGAT 1034  
DB 961 AATATATATTTTCTTTTATGAGGGTGACCCGTGTTACTACGAGAAATGTAATCTGTTGAT 1020  
QY 1035 CAACCTTTTATCTCACCATTTTATATATATATGTTTCAGGGCCAAATTTATGATAAATTA 1094  
DB 1021 CAACCTTTTATCTCACCATTTTATATATATATGTTTCAGGGCCAAATTTATGATAAATTA 1080  
QY 1095 ACTGAACCTTAAGAACCAAGAGATGCGCAACTTTATTTAAGGATAAAGAGCTTGATTTAT 1154  
DB 1081 ACTGAACCTTAAGAACCAAGAGATGCGCAACTTTATTTAAGGATAAAGAGCTTGATTTAT 1140  
QY 1155 GGTGTAGATATATACATCTCTGTTTATTTATGTAAGAAATGCGAAGAGGTCATGTATC 1214  
DB 1141 GGTGTAGATATATACATCTCTGTTTATTTATGTAAGAAATGCGAAGAGGTCATGTATC 1200  
QY 1215 TACGAGGAGGTTAAACAAATCATCAAGGGAATCATTTAGAAATTTCTTAAAAAGTACTCGTT 1274  
DB 1201 TACGAGGAGGTTAAACAAATCATCAAGGGAATCATTTAGAAATTTCTTAAAAAGTACTCGTT 1260  
QY 1275 AAAGTATCAATCGATGGTATCCAAAGCCATCATTTGATTTGAAACCAATTAATAAATG 1334  
DB 1261 AAAGTATCAATCGATGGTATCCAAAGCCATCATTTGATTTGAAACCAATTAATAAATG 1320  
QY 1335 GTAACTGCTCAAGAAATTAGACTATATAAGTTAGAAATATCTTTACAGATAAATTAAGCAACTA 1394  
DB 1321 GTAACTGCTCAAGAAATTAGACTATATAAGTTAGAAATATCTTTACAGATAAATTAAGCAACTA 1380  
QY 1395 TATACATAATGAGACCTTCAAAATPATGAACCTGATATATAAGTTTATCATCTTAAGATAA 1454  
DB 1381 TATACATAATGAGACCTTCAAAATPATGAACCTGATATATAAGTTTATCATCTTAAGATAA 1440  
QY 1455 GAAAGTTTTTGGTTGATTTTTCCTCGAACCAAGAAATTTACTCAATCTAAATATCTTATG 1514

Db 1441 GAAAGCTTTTGGTTGATTTTCCCTGACGAGAAATTAATCAATCTAAATATCTTATG 1500  
Qy 1515 ATATATAAGTAATGAACGCTTGACTCAACACAGCCAAATTAAGTCTACCTAACA 1574  
Db 1501 ATATATAAGTAATGAACGCTTGACTCAACACAGCCAAATTAAGTCTACCTAACA 1560  
Qy 1575 ACCAAGTAACCTTTTGGCTTTTGGCAACCTTACCTACTGCTGGAATTTAGAAATTTATTGC 1634  
Db 1561 ACCAAGTAACCTTTTGGCTTTTGGCAACCTTACCTACTGCTGGAATTTAGAAATTTATTGC 1620  
Qy 1635 AATCTTTTATTAATGTAAGAAACCGCTCATTTGTATGAGCGGTTTGTCTTATCTAAGGA 1694  
Db 1621 AATCTTTTATTAATGTAAGAAACCGCTCATTTGTATGAGCGGTTTGTCTTATCTAAGGA 1680  
Qy 1695 GCTTTACCTCTTAAGCTGCAAAATTTTAAATGTTGGAATTTTGTATTGTCTATTGTAT 1754  
Db 1681 GCTTTACCTCTTAAGCTGCAAAATTTTAAATGTTGGAATTTTGTATTGTCTATTGTAT 1740  
Qy 1755 TTGATGGTAATCCCATTTTTCGACAGACATCGTGTGCGCACTCTTAACACCAAAATCAT 1814  
Db 1741 TTGATGGTAATCCCATTTTTCGACAGACATCGTGTGCGCACTCTTAACACCAAAATCAT 1800  
Qy 1815 AGACAGGAGCTGTAGCTTAGCAACTATTATTATCGTC 1851  
Db 1801 AGACAGGAGCTGTAGCTTAGCAACTATTATTATCGTC 1837

RESULT 6

ABN84229  
ID ABN84229 standard; CDNA; 1837 BP.  
XX AC ABN84229;  
XX DT 23-SEP-2002 (first entry)  
XX DE Streptococcal pyrogenic exotoxin A vaccine SPEa42 coding sequence.  
XX KW Exotoxin A; SPEa; SPEa42; superantigen; antigen; toxin; vaccine;  
XX KW attenuation; mutant; gene; ss.  
XX OS Streptococcus pyogenes.  
XX FH Location/Qualifiers  
XX FT 814..1569  
XX FT /\*tag= a  
XX FT /\*product= "SPEa42"

XX PN US6399332-B1.

XX PD 04-JUN-2002.

XX PF 01-SEP-1998; 98US-00144776.

XX PR 25-JUN-1997; 97US-00882431.

XX PA (USSA ) US SEC OF ARMY.

XX PI Ulrich RG, Olson MA, Bavari S;

XX DR WPI; 2002-546281/58.

XX DR P-PSDB; ABB79508.

XX Novel isolated and purified superantigen toxin DNA fragment which has  
XX been genetically altered, useful for producing vaccine for treatment of  
XX superantigen toxin-associated bacterial diseases.

XX PS Disclosure; Col 61-63; 46pp; English.

XX The present sequence is the coding sequence of Streptococcus pyogenes  
XX vaccine SPEa42. The vaccine differs from the native SPEa sequence by  
XX substitution of the Leu-42 residue by Arg. This mutation is expected to

CC disrupt contact between the toxin and the HLA-DR receptor, reducing DRI  
CC binding. SPEa42 can be expressed as a recombinant protein in Escherichia  
CC coli as a secreted protein or as a cytoplasmic product. No indicators of  
CC toxicity have been detected for the purified recombinant protein, and  
CC vaccine studies demonstrate that SPEa42 is highly antigenic, inducing  
CC protective immunity in a mouse animal model. The attenuated superantigen  
CC can be used to protect against superantigen toxin infections. Methods of  
CC producing and using altered superantigen toxins as vaccines, and in  
CC diagnosis and therapy, are provided by the invention. A multivalent  
CC vaccine consisting of altered superantigen toxins from SEA, SEB, SEC-1,  
CC TSST-1 and SPEa is predicted to provide protective immunity against the  
CC majority of bacterial superantigen toxins  
XX  
XX Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;

Query Match 99.0%; Score 1832.2; DB 6; Length 1837;  
Best Local Similarity 99.8%; Pred. No. 4.7e-286;  
Matches 1834; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 15 TCATGTTTCACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGTCTATCTTGAAC 74  
Db 1 TCATGTTTCACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGTCTATCTTGAAC 60  
Qy 75 AGGTGCAACATAGATTAGGGCATGGAGATTACCGAGCAACTATGAACGTATATATCTAC 134  
Db 61 AGGTGCAACATAGATTAGGGCATGGAGATTACCGAGCAACTATGAACGTATATATCTAC 120  
Qy 135 ATCAGCGAATCGGCATTTGATGACATGGAATTAATCAATCAATTTGTTACTACACAG 194  
Db 121 ATCAGCGAATCGGCATTTGATGACATGGAATTAATCAATCAATTTGTTACTACACAG 180  
Qy 195 CAACTAGATTGACAACTAATTTCTCAACAAACGTTAATTTTAAACAACATTCAGTAATCCC 254  
Db 181 CAACTAGATTGACAACTAATTTCTCAACAAACGTTAATTTTAAACAACATTCAGTAATCCC 240  
Qy 255 ACCAGCTCCATCAATCGTTACCGTAAGTAATCAATACTTACTTAAACCTTGTATACATCA 314  
Db 241 ACCAGCTCCATCAATCGTTACCGTAAGTAATCAATACTTACTTAAACCTTGTATACATCA 300  
Qy 315 GGTGTTTTCTTTTGTCTTGTTCATGAGTTACCAATCTTCTATATTTATTTGCAACTAA 374  
Db 301 GGTGTTTTCTTTTGTCTTGTTCATGAGTTACCAATCTTCTATATTTATTTGCAACTAA 360  
Qy 375 ATTGACAACTCTTCAATTTTCTGCTACTCAAGTTTCTTCAATTTGATATAGTCT 434  
Db 361 ATTGACAACTCTTCAATTTTCTGCTACTCAAGTTTCTTCAATTTGATATAGTCT 420  
Qy 435 AATTCCACCATCACTTCTTCCACTCTCTACCGTCACCACTTCTCATCTCTCTCATCTTT 494  
Db 421 AATTCCACCATCACTTCTTCCACTCTCTACCGTCACCACTTCTCATCTCTCTCATCTTT 480  
Qy 495 TCGTGTGGTAACACATAATCAAAATATCTTTCCGTTTTTACGCACTATCGTACTGTGCA 554  
Db 481 TCGTGTGGTAACACATAATCAAAATATCTTTCCGTTTTTACGCACTATCGTACTGTGCA 540  
Qy 555 CCTAAATATACCGCTTATCAATCGCTTCTTAAACTCATCTATATATAACATTTTCAT 614  
Db 541 CCTAAATATACCGCTTATCAATCGCTTCTTAAACTCATCTATATATAACATTTTCAT 600  
Qy 615 CCTCCTACCTATCTATTCGTAAGAAATAAATAAATACTATGTTTTTTTGTATTTTAT 674  
Db 601 CCTCCTACCTATCTATTCGTAAGAAATAAATAAATACTATGTTTTTTTGTATTTTAT 660  
Qy 675 AATAAATATTAATAAGTAAATGTTTTTAAATAATACAAATTTTATCTATTATATA 734  
Db 661 AATAAATATTAATAAGTAAATGTTTTTAAATAATACAAATTTTATCTATTATATA 720  
Qy 735 GTTAGCTATTTTTCATTGTTAGTAATATTGGCAATTTGTAATACCTTTTAAATCTAG 794  
Db 721 GTTAGCTATTTTTCATTGTTAGTAATATTGGCAATTTGTAATACCTTTTAAATCTAG 780  
Qy 795 AGGAGACCCAGATATAAATGAGGATATTAATGGAACCAATTAAGATTTTCAAG 854

781 AGGAGAACCCAGATATATAAAATGGAGGAATATTAATGGAACAAATAAAAAAGTATTGAAG 840  
855 AAAATGATATTTTGTGTTTGTAGTACATTTCTTGAGCTAAACAATCTCGAAGAGGTATTT 914  
841 AAAATGGTATTTTGTGTTTGTAGTACATTTCTTGAGCTAAACAATCTCGAAGAGGTATTT 900  
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901 GGTCAACAGACCCCGATCCAGCCAACTTACAGATCTAGTTAGTTAAAAACCTTCAA 960  
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961 AATATATATTTTCTTTATGAGGGTGAACCTGTTACTCAGGAGATGTGAATCTGTTGAT 1020  
1035 CAACCTTTTATCTCACCATTATATATATATATATGTTTTCAGGGCCAAATTTATGATAAAATTTAAA 1094  
1021 CAACCTTTTATCTCACCATTATATATATATATATGTTTTCAGGGCCAAATTTATGATAAAATTTAAA 1080  
1095 ACTGAATCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATATAAAAGTTGATATTTAT 1154  
1081 ACTGAATCTTAAGAACCAAGAGATGGCACTTTATTTAAGGATATAAAAGTTGATATTTAT 1140  
1155 GGTGTAGATATATACCATCTCTGTTTATTTATGTAATGCAAGAGGAGTGCATGTATC 1214  
1141 GGTGTAGATATATACCATCTCTGTTTATTTATGTAATGCAAGAGGAGTGCATGTATC 1200  
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1201 TACGAGGGGTAAACAAATCATGAAGGAATCATTTAGAAATTCCTAAAGATAGTCTGTT 1260  
1275 AAAGTATCAATCGATGATGATCAAGGCTTATCATTTGATGTAATGAAACAAATAAAAAATG 1334  
1261 AAAGTATCAATCGATGATGATCAAGGCTTATCATTTGATGTAATGAAACAAATAAAAAATG 1320  
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1321 GTAACTGCTCAAGAAATAGACTATATAAGTTAGAAATATCTTACAGATATAAGCAACTA 1380  
1395 TATCTAAATGACCTTCTAAATATGAATGAACCTGATATATAAGTTCACTAAGTAATAA 1454  
1381 TATCTAAATGACCTTCTAAATATGAATGAACCTGATATATAAGTTCACTAAGTAATAA 1440  
1455 GAAAGTTTTTGTGTTGATTTTTTCCCTGAACAGAAATTTACTCAATCTAAATATCTTATG 1514  
1441 GAAAGTTTTTGTGTTGATTTTTTCCCTGAACAGAAATTTACTCAATCTAAATATCTTATG 1500  
1515 ATATATAAGATATGAAGCGTTGACTCAACACAGCAATTTGAAGTCTACCTTAA 1574  
1501 ATATATAAGATATGAAGCGTTGACTCAACACAGCAATTTGAAGTCTACCTTAA 1560  
1575 ACCAAGTAACTTTTGTGTTTGGCAACCTTACCTACTGCTGGATTTAGAAATTTTATTC 1634  
1561 ACCAAGTAACTTTTGTGTTTGGCAACCTTACCTACTGCTGGATTTAGAAATTTTATTC 1620  
1635 AATCTTTTATTAATGTAAAAACCGCTCATTTGATGAGCGGTTTGTCTTATCTAAAGGA 1694  
1621 AATCTTTTATTAATGTAAAAACCGCTCATTTGATGAGCGGTTTGTCTTATCTAAAGGA 1680  
1695 GCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGATTTTTTGTATTTGCTTATTTGAT 1754  
1681 GCTTTACCTCTTAATGCTGCAAAATTTTAAATGTTGATTTTTTGTATTTGCTTATTTGAT 1740  
1755 TTGATGGGTAAATCCCATTTTTCAGACAGACATCGTCGTCACCTCTAAACACCAAAATCAT 1814  
1741 TTGATGGGTAAATCCCATTTTTCAGACAGACATCGTCGTCACCTCTAAACACCAAAATCAT 1800  
1815 AGACAGAGCTGTAGCTTAGCAACTATTTTATTCGTC 1851  
1801 AGACAGAGCTGTAGCTTAGCAACTATTTTATTCGTC 1837

ID XX ACA61184 standard; DNA; 1837 BP.  
AC AC ACA61184;  
DT 11-AUG-2003 (first entry)  
XX DNA encoding streptococcal pyrogenic exotoxin A.  
XX Pyrogenic exotoxin A; ds; superantigen-associated bacterial infection;  
XX superantigen toxin; gene; vaccine.  
XX Streptococcus sp.  
FH Key Location/Qualifiers  
FT CDS 814..1569  
FT /tag a  
FT /product= "Pyrogenic exotoxin A"  
XX US2003009015-A1.  
XX 09-JAN-2003.  
XX 25-JUN-1997; 97US-00882431.  
XX 25-JUN-1997; 97US-00882431.  
XX (ULRI/) ULRI R G.  
XX (OLSO/) OLSON M A.  
XX (BAVA/) BAVARI S.  
XX Ulrich RG, Olson MA, Bavari S;  
XX WPI: 2003-401542/38.  
XX P-PSDB; ABU10088.  
XX New superantigen toxin and/or DNA fragment with an altered binding of the  
XX encoded altered toxin to either MHC class II or T cell antigen receptor,  
XX useful for treating or ameliorating superantigen-associated bacterial  
XX infection.  
XX Claim 9; Page 32-34; 50pp; English.  
XX The invention relates to an isolated and purified superantigen toxin  
XX and/or DNA fragment, which has been altered so that the binding of the  
XX encoded toxin to either major histocompatibility complex (MHC) class II  
XX or T cell antigen receptor is altered. The superantigen toxins, DNA  
XX fragments, and vaccines are useful for treating or ameliorating  
XX superantigen-associated bacterial infection. The DNA fragments are  
XX particularly useful for producing vaccine against superantigen toxin  
XX infections. The transformed host cells are useful for analyzing the  
XX effectiveness of drugs and agents that affect the binding of  
XX superantigens to MHC class II or T-cell antigen receptors. The present  
XX sequence represents DNA encoding streptococcal pyrogenic exotoxin A  
SQ Sequence 1837 BP; 632 A; 318 C; 249 G; 638 T; 0 U; 0 Other;  
Query Match 99.0%; Score 1832.2; DB 7; Length 1837;  
Best Local Similarity 99.8%; Pred. No. 4.7e-286; Indels 0; Gaps 0;  
Matches 1834; Conservative 0; Mismatches 3;  
QY 15 TCATGTTTGGACAGCTTATCATCGATAGCTTACTTTTCGAATCAGGTCTATCTTGAAC 74  
Db 1 TCATGTTTGGACAGCTTATCATCGATAGCTTACTTTTCGAATCAGGTCTATCTTGAAC 60  
QY 75 AGGTCAACATAGATTAGGCGATGAGATTTACAGACAACTATGACGTATATCTAC 134  
Db 61 AGGTCAACATAGATTAGGCGATGAGATTTACAGACAACTATGACGTATATCTAC 120  
QY 135 ATCAGCAATCGCAATTTGATGACATTCGAACTAAATTCATTTGTTTACTTAACAAG 194  
Db 121 ATCAGCAATCGCAATTTGATGACATTCGAACTAAATTCATTTGTTTACTTAACAAG 180  
QY 195 CAACATAGATTGACAACTAATTTCTCAACAAAGCTTAAATTTAAACAACATTCAGTAACCTCC 254



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Db 181 CAACTAGATTGACAACTAAATCTCAACAAACGGTTAAATTTAAACAACATCTCAAGTAACTCC 240
Qy 255 ACCAGCTCCATCAATGCTTACCGTAAGTAATCAATCACTTAACAACTTGTACATCAA 314
Db 241 ACCAGCTCCATCAATGCTTACCGTAAGTAATCAATCACTTAAACCTTGTACATCAA 300
Qy 315 GGTATTTTCTTTTGTCTGTCTGATGAGTTACCAATACTTTCTATATATTGACAACATA 374
Db 301 GGTATTTTCTTTTGTCTGTCTGATGAGTTACCAATACTTTCTATATATTGACAACATA 360
Qy 375 ATTGACAACTCTTCAATATATTTTCTGCTACTCAAGAGTTTCTTCAATTTGATATAGTCT 434
Db 361 ATTGACAACTCTTCAATATATTTTCTGCTACTCAAGAGTTTCTTCAATTTGATATAGTCT 420
Qy 435 AATTCCACCACTCACTTCTCCACTCTCTTACCGTCAAACTTCATCATCTCTCACTTTT 494
Db 421 AATTCCACCACTCACTTCTCCACTCTCTTACCGTCAAACTTCATCATCTCTCACTTTT 480
Qy 495 TCGTGTGTAAACANATCAATCAATCTTCCGTTTAACTCATCTATATATAACATATTTTCA 554
Db 481 TCGTGTGTAAACANATCAATCAATCTTCCGTTTAACTCATCTATATATAACATATTTTCA 540
Qy 555 CCTAAATATACCCCTTATCAATCGTCTTCTTAACTCATCTATATATAACATATTTTCA 614
Db 541 CCTAAATATACCCCTTATCAATCGTCTTCTTAACTCATCTATATATAACATATTTTCA 600
Qy 615 CCTCTACTATCTATCTGTAAGTAATGCGTGAATTTGTAATTAACCTTTTGTATTTTAT 674
Db 601 CCTCTACTATCTATCTGTAAGTAATGCGTGAATTTGTAATTAACCTTTTGTATTTTAT 660
Qy 675 AATAAATATTAATATAGTTAATGTTTAAATATACAAATTTATTTCTATTTTATA 734
Db 661 AATAAATATTAATATAGTTAATGTTTAAATATACAAATTTATTTCTATTTTATA 720
Qy 735 GTTAGCTATTTTTCATTTGTTAGTAATATGCGTGAATTTGTAATTAACCTTTTAAATCTAG 794
Db 721 GTTAGCTATTTTTCATTTGTTAGTAATATGCGTGAATTTGTAATTAACCTTTTAAATCTAG 780
Qy 795 AGGAGAACCCAGATATAAATGGAGGAATATTAATGGAAACAAATAAAGAGTATTCAG 854
Db 781 AGGAGAACCCAGATATAAATGGAGGAATATTAATGGAAACAAATAAAGAGTATTCAG 840
Qy 855 AAAATGGTATTTTGTGTTTGTAGTACATTTCTTGACCTAAACAATCTCGCAAGAGTATTT 914
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Db 901 GCTCAACAGACCCCGATCCAAAGCAACTTCACAGATCTAGTTAGTTAAAGCCTTCAA 960
Qy 975 AATATATATTTTCTTTATGAGGTGACCTGTTACTACGAGAATGTGAATCTGTTGAT 1034
Db 961 AATATATATTTTCTTTATGAGGTGACCTGTTACTACGAGAATGTGAATCTGTTGAT 1020
Qy 1035 CAACTTTTATCTCACCATTAATATATATGTTTTCAGGGCCAAATTAATGATAAATAA 1094
Db 1021 CAACTTTTATCTCACCATTAATATATATGTTTTCAGGGCCAAATTAATGATAAATAA 1080
Qy 1095 ACTGAACTTAAGAACCAAGAGATGCACTTTTATTTAAAGGATAAAGACGTTGATTTAT 1154
Db 1081 ACTGAACTTTAAGAACCAAGAGATGCACTTTTATTTAAGGATAAAGACGTTGATTTAT 1140
Qy 1155 GGTGTAGAAATATTACCATCTCTGTTTATTTATGTGAATATGCAAGAGGTGCATGTATC 1214
Db 1141 GGTGTAGAAATATTACCATCTCTGTTTATTTATGTGAATATGCAAGAGGTGCATGTATC 1200
Qy 1215 TACGGAGGGGTAAACATCAATGAGGATCATCTTTAGAAATTCCTAAAGAGATAGTCGTT 1274
Db 1201 TACGGAGGGGTAAACATCAATGAGGATCATCTTTAGAAATTCCTAAAGAGATAGTCGTT 1260
Qy 1275 AAAGTATCAATCGATGGTATCCAAAGCCTTATCTGATTTGAAACAAATAAAGAAATG 1334
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Db 1261 AAAGTATCAATCGATGGTATCCAAAGCCTATCTATTTGATATTGAAACAATATAAATG 1320
Qy 1335 GTAACCTGCTCAAGAAATTAGACTATATAAGTTAGAAAAATATCTTACAGATAAAGCACTA 1394
Db 1321 GTAACCTGCTCAAGAAATTAGACTATATAAGTTAGAAAAATATCTTACAGATAAAGCACTA 1380
Qy 1395 TATACATAATGACCTTCTAATAATGAACTGAACTATATAAAGTTTATACCTTAAGATAA 1454
Db 1381 TATACATAATGACCTTCTAATAATGAACTGAACTATATAAAGTTTATACCTTAAGATAA 1440
Qy 1455 GAAAGTTTTTGGTTTGAATTTTTTCCCTGAACCAAGAAATTTACTCAATCTAAATATCTTATG 1514
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Qy 1515 ATATATAAGATAATGAAACCGTTGACCTCAACACACCAAGCCAAATTTGAAGTCTACCTAACA 1574
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Qy 1575 ACCAAGTAACTTTTGGCTTTTGGCAACCTTACTACTGCTGGAATTTAGAAATTTTATTGTC 1634
Db 1561 ACCAAGTAACTTTTGGCTTTTGGCAACCTTACTACTGCTGGAATTTAGAAATTTTATTGTC 1620
Qy 1635 AATCTTTTATTAATGTAAGAAACCGCTCATTTGATGAGCGGTTTGTCTTATCTAAGGA 1694
Db 1621 AATCTTTTATTAATGTAAGAAACCGCTCATTTGATGAGCGGTTTGTCTTATCTAAGGA 1680
Qy 1695 GCTTTACCTCCCTAAATGCTGCAAAATTTTAAATGTTGGATTTTGTATTTGTCTATTGTAT 1754
Db 1681 GCTTTACCTCCCTAAATGCTGCAAAATTTTAAATGTTGGATTTTGTATTTGTCTATTGTAT 1740
Qy 1755 TTGATGGGTAATCCCAATTTTTCGACAGACATCGTGTGTCACCTCTTAACACCAAAATCAT 1814
Db 1741 TTGATGGGTAATCCCAATTTTTCGACAGACATCGTGTGTCACCTCTTAACACCAAAATCAT 1800
Qy 1815 AGACAGAGCTGTAGCTTAGCAACTATTTTATTCGTC 1851
Db 1801 AGACAGAGCTGTAGCTTAGCAACTATTTTATTCGTC 1837

RESULT 8
AAD56771
ID AAD56771 standard; DNA; 1837 bp.
XX
AC AAD56771;
XX
DT 06-OCT-2003 (first entry)
XX
DE Streptococcus pyogenes pyrogenic exotoxin A (spea) DNA.
XX
KW Superantigen toxin; vaccine; infection; pyrogenic exotoxin A; SpeA;
  gene therapy; gene; ds.
XX
OS Streptococcus pyogenes.
XX
FH Key Location/Qualifiers
CDS 814..1569
FT /tag= a
FT /product= "Streptococcus pyogenes SpeA protein"
FT /transl_except= (pos:901..903, aa:Met)
FT /note= "This translational exception occurs only when
  decoding SEQ ID NO: 26 (AAE37687)"
FT sig_peptide 814..900
FT /tag= b
FT mat_peptide 901..1566
FT /tag= c
FT /product= "Streptococcus pyogenes mature SpeA protein"
XX
PF WO2003056075-A1.
XX 10-JUL-2003.
XX
PP 26-NOV-2001; 2001WO-US046540.
XX
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Db 1741 TTGATGGGTATCCCATTTTTCGACAGACATCGTGTGCCACCTCTACACCAAAATCAT 1800

QY 1815 AGACAGGAGCTGTAGCTTAGCAACTATTTTATCGTC 1851

Db 1801 AGACAGGAGCTGTAGCTTAGCAACTATTTTATCGTC 1837

RESULT 9

ACD28901

ID ACD28901 standard; DNA; 1837 BP.

AC ACD28901;

XX

DT 27-AUG-2003 (first entry)

XX

DE Streptococcus pyrogenic toxin a L42R mutant, DNA.

XX

KW SPEa; streptococcus pyrogenic enterotoxin a; gene; mutant; vaccine; ds;

KW superantigen toxin; MHC; superantigen-associated bacterial infection;

XX bacterial infection; antibacterial.

XX

OS Streptococcus sp.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 814..1569

FT /\*tag= a

FT /product= "SPEa L42R"

FT sig\_peptide 814..903

FT /\*tag= b

FT mat\_peptide 904..1566

FT /\*tag= c

FT /label= Mature\_SPEa\_L42R

XX

US2003036644-A1.

XX

20-PEB-2003.

XX

26-NOV-2001; 2001US-00002784.

XX

25-JUN-1997; 97US-00882431.

PR 01-SEP-1998; 98US-00144776.

XX

(ULRI/) ULRICH R G.

XX

Ulrich RG;

XX

WPI; 2003-492125/46.

DR P-PSDB; ABU62331.

XX

New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.

XX

Claim 4; Page 36-37; 68pp; English.

XX

The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection), an antiserum against superantigen-associated bacterial infection, an antiserum isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated streptococcal enterotoxin A, B, C1 (SEA, SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and SPEb). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present

CC sequence encodes the L42R (with reference to the mature protein) mutant of SPEa

XX

SQ Sequence 1837 BP; 633 A; 318 C; 248 G; 638 T; 0 U; 0 Other;

Query Match 98.9%; Score 1830.6; DB 8; Length 1837;

Best Local Similarity 99.8%; Pred. NO. 8.6e-286;

Matches 1833; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 15 TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGCTCTATCTTGAAAC 74

Db 1 TCATGTTTGACAGCTTATCATCGATAAGCTTACTTTTCGAATCAGGCTCTATCTTGAAAC 60

QY 75 AGGTGCAACATAGATTAGGCGATGGAGATTACCGACAACTATGAACGTATATATCTCAC 134

Db 61 AGGTGCAACATAGATTAGGCGATGGAGATTACCGACAACTATGAACGTATATATCTCAC 120

QY 135 ATCACCGAATCGCAATTCATGACATTCGAACTTAATTCATCAATTCCTTACTACCAAG 194

Db 121 ATCACCGAATCGCAATTCATGACATTCGAACTTAATTCATCAATTCCTTACTACCAAG 180

QY 195 CAAGTAGATTGACAACTAATTTCTCAACAAACGTTAATTTAAACAACATTCAGTAATCCC 254

Db 181 CAAGTAGATTGACAACTAATTTCTCAACAAACGTTAATTTAAACAACATTCAGTAATCCC 240

QY 255 ACCAGCTCCATCAATGCTTACCGTAAGTAATCATTAACCTTACTAABACCTTGTATACATA 314

Db 241 ACCAGCTCCATCAATGCTTACCGTAAGTAATCATTAACCTTACTAABACCTTGTATACATA 300

QY 315 GGTGTTTCTTTTGTCTTGTTCATGAGTTACCAATCTTCTATATATTGACAACTAA 374

Db 301 GGTGTTTCTTTTGTCTTGTTCATGAGTTACCAATCTTCTATATATTGACAACTAA 360

QY 375 ATTGACAACTCTTCAATTAATTTTCTGCTACTCAAGTTTCTTCAATTTGATATAGTCT 434

Db 361 ATTGACAACTCTTCAATTAATTTTCTGCTACTCAAGTTTCTTCAATTTGATATAGTCT 420

QY 435 AATTCCACCATCACTTCTTCCACTCTCTACCGTCACAACTTCACTCACTCTCTCACTTTT 494

Db 421 AATTCCACCATCACTTCTTCCACTCTCTACCGTCACAACTTCACTCACTCTCTCACTTTT 480

QY 495 TCGTGTGGTAAACATAAATCAAAATATCTTTCGGTTTTAGGCACTATCGTACTGTGTC 554

Db 481 TCGTGTGGTAAACATAAATCAAAATATCTTTCGGTTTTAGGCACTATCGTACTGTGTC 540

QY 555 CCTAAAATATACCCCTTATCAATCGCTTCTTAAACTCATCTATATATAAATATTCAT 614

Db 541 CCTAAAATATACCCCTTATCAATCGCTTCTTAAACTCATCTATATATAAATATTCAT 600

QY 615 CTTCTACCTATCTATTCGTAAGAAATATAAATACTATTTGTTTTTTTGTATTTTAT 674

Db 601 CTTCTACCTATCTATTCGTAAGAAATATAAATACTATTTGTTTTTTTGTATTTTAT 660

QY 675 AATAAATATTAATTAATTAAGTTAATGTTTTTAAATATATAAATTTTCTTATTTATA 734

Db 661 AATAAATATTAATTAATTAAGTTAATGTTTTTAAATATATAAATTTTCTTATTTATA 720

QY 735 GTTAGCTATTTTTCATTTGTAGTAATTAATGTTGAATTTGTAATTAACCTTTTAAATCTAG 794

Db 721 GTTAGCTATTTTTCATTTGTAGTAATTAATGTTGAATTTGTAATTAACCTTTTAAATCTAG 780

QY 795 AGGAGACCCAGATATAAATGAGGAATTAATGGAACAACTAATAAAGTATTGAAG 854

Db 781 AGGAGACCCAGATATAAATGAGGAATTAATGGAACAACTAATAAAGTATTGAAG 840

QY 855 AAAATGTTATTTTGTGTTTGTAGTGACATTTCTTGGACTTAACTCTCGCAAGAGGTATTT 914

Db 841 AAAATGTTATTTTGTGTTTGTAGTGACATTTCTTGGACTTAACTCTCGCAAGAGGTATTT 900

QY 915 GCTCAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAA 974

Db 901 GCTCAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAA 960



the US patnet office website at  
"seqdata.uspto.gov/sequence.html?docID=20020177551"

Sequence 1031 BP; 381 A; 146 C; 162 G; 342 T; 0 U; 0 Other;

Query Match 48.2%; Score 892.8; DB 7; Length 1031;  
Best Local Similarity 95.7%; Pred. No. 7.2e-135;  
Matches 993; Conservative 37; Indels 8; Gaps 7;

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DB 1 ATGTGTTAATAATATGTTGTAATTTGTAATTAACCTTTTAAATCTAGAGGAGAACCCAGATA 60  
QY 810 TAAATGGAGGAATATTAATGGAAACATATAAAGATTTTGAAGAAAATGGTATTTTTT 869  
DB 61 TAAATGGAGGAATATTAATGGAAACATATAAAGATTTTGAAGAAAATGGTATTTTTT 120  
QY 870 GTTTTGTGACATTTCTTGGACTTAACATCTCGCAAGAGGTATTTGCTCAACAGACCCC 929  
DB 121 GTTTTGTGAAATTTCTTGGACTTAACATCTCGCAAGAGGTATTTGCTCAACAGACCCC 180  
QY 930 GATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAATATATATTTTCTT 989  
DB 181 AAGCCAGCCAACTTACAAAGATCTAATTTAGTT-AAAACCTTCAAAATATATATTTTCTT 239  
QY 990 TATGAGGTGACCT-GTTTACTCAGAGATGTGAATCTGTTGATCAACTTTTATCTCA 1048  
DB 240 TATGAGGTGACCTGGTTTACTCAGAGATGTGAATCTGTTGATCAACTTTTATCTCA 299  
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DB 300 CGATTTAATATATATGTTTTCAGGGCCAAATATGATTAATTAATAAATGAACTTAAAGAA 359  
QY 1109 CCAGAGATGGCAACTTTTAAAGATTAACAGCTTGTATTTATGTTGATGAATATTA 1168  
DB 360 CCAAGAGATGGCAACTTTTAAAGATTAACAGCTTGTATTTATGTTGATGAATATTA 419  
QY 1169 CCATCTCTGTTATTTATGTAATAATCCAGAAAGGAGTGTATCTACGGAGGGTAAAC 1228  
DB 420 CCATCTCTGTTATTTATGTAATAATCCAGAAAGGAGTGTATCTACGGAGGGTAAAC 479  
QY 1229 AATATCATGAGGAATCATTAGAAATTCCTTAAAGATAGTTCGTTAAAGTATCAATCGA 1288  
DB 480 AATATCATGAGGAATCATTAGAAATTCCTTAAAGATAGTTCGTTAAAGTATCAATCGA 539  
QY 1289 TGGTATCCAAAGCTTATCATTTGATATGAAACAAATATAAATAATGTTAACTGCTCAAGA 1348  
DB 540 TGGTATCCAAAGCTTATCATTTGATATGNA--CAATTAATAATGTTAACTGCTCAAGA 597  
QY 1349 ATTAGACTATAAGTTAGAAAATATCTTACAGATAATTAAGCAACTATATATATGGACC 1408  
DB 598 ATTAG-CTATACAGTTAGAAAATATCTTACAGATAATTAAGCAACTATATATATGGACC 656  
QY 1409 TTCTAATATGAACCTGGATATATAAGTTTCACTACCTTAAGATAAAGAAAGTTTGGTT 1468  
DB 657 TTCTAATATGAACCTGGATATATAAGTTTCACTACCTTAAGATAAAGAAAGTTTGGTT 716  
QY 1469 TGAATTTTTCCCTGAACCAAGATTTACTCAATCTAATTAATCTTATGATATATAAGATTA 1528  
DB 717 TGAATTTTTCCCTGAACCAAGATTTACTCAATCTAATTAATCTTATGATATATAAGATTA 776  
QY 1529 TGAACGCTTGACTCAACACAGCCAAATTTGAAGTCTACCTTAACCAAGCAAGTAACTTTT 1588  
DB 777 TGAACGCTTGACTCAACACAGCCAAATTTGAAGTCTACCTTAACCAAGCAAGTAACTTTT 835  
QY 1589 TGCTTTTGGCAACCTTACCTACTGCTGGATTTAGAAAATTTTATGCAATCTTTTATTA 1648  
DB 836 TGCTTTTGGCAACCTTACCTACTGCTGGATTTAGAAAATTTTATGCAATCTTTTATTA 895  
QY 1649 TGTAAAAACGCTCATTTGATGAGCGTTTGTCTTATCTTAAGGAGCTTTTACCTCTAA 1708  
DB 896 TGTAAAAA-CGCTCATTTGATGAGCGGTTTGTCTTATCTTAAGGAGCTTTTACCTCTAA 954

QY 1709 TGCTGCAAAATTTAAATGTTGATTTTGTATTTGTTCTATTTGTTATTTGATGGTAATCC 1768  
DB 955 TGCTGCAAAATTTAAATGTTGATTTTGTATTTGTTCTATTTGTTATTTGATGGTAATCC 1013  
QY 1769 CATTTTTCGACAGACATC 1786  
DB 1014 CATTTTTCGACAGACATC 1031

RESULT 11  
AAH01002  
ID AAH01002 standard; DNA; 756 BP.  
XX AAH01002;  
XX AC  
XX AAH01002;  
DT 24-JUL-2001 (first entry)  
XX Unidentified nucleotide sequence SEQ ID NO:993.

Species specific; genus specific; family specific; probe; detection;  
identification; algal; archaeal; bacterial; fungal; parasiticol;  
microorganism; diagnosis; translation elongation factor Tu; toxin;  
translation elongation factor G; RecA recombinase; resistance;  
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;  
primer; ds.

Unidentified.

WO200123604-A2.

05-APR-2001.

28-SEP-2000; 2000WO-CA0007150.

28-SEP-1999; 99CA-0283458.

19-MAY-2000; 2000CA-02307010.

(INFS-) INEBPTIO DIAGNOSTIC (IDI) INC.

Bergerson MG, Boissinot M, Huletsky A, Menard C, Ouellette M;  
Picard FJ, Roy PH;

WPI, 2001-245006/25.

Nucleic acid sequences are used to generate universal probes and primers  
which can be used to identify and detect the presence of algal, archaeal,  
bacterial, fungal and parasiticol species in a test sample.

Disclosure; Page 957; 1580pp; English.

The present invention describes a method for generating a repertory of  
nucleic acids of tuf, fus, apd and/or recA genes from which probes  
and/or primers are derived. The method comprises amplifying the nucleic  
acids of determined algal, archaeal, bacterial, fungal and parasiticol  
species with a combination of defined primer pairs. The method can be  
used for producing probes and/or primers for detecting one or more  
related microorganisms e.g. algae, archaea, bacteria, fungi and  
parasites, for universal detection and for specific and ubiquitous  
detection and identification of an algal, archaeal, bacterial, fungal and  
parasiticol species, genus, family and group. A nucleic acid (I) obtained  
using the method of the invention can be used for the universal detection  
of any bacterium, fungus or parasite in a sample and for the detection of  
at least one antimicrobial agent resistance gene or at least one toxin  
gene. hexA nucleic acids are used for the specific and ubiquitous  
detection and for identification of Streptococcus pneumoniae. (I) can be  
used to design a therapeutic agent which is effective against  
microorganisms. Microbial species or genus or family or phylum or group  
which can be detected include Abiotrophia adiacens, Bordetella sp.,  
Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,  
Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria  
gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster  
results than substrate specificity tests as results can be determined in  
an hour and improved accuracy is also achieved. AAH00010 to AAH002304

CC represent nucleotide sequences and primers/probes which are given in the  
XX exemplification of the present invention  
SQ Sequence 756 BP; 297 A; 110 C; 118 G; 231 T; 0 U; 0 Other;

Query Match 40.8%; Score 754.4; DB 4; Length 756;  
Best Local Similarity 99.9%; Pred. No. 1.4e-112;  
Matches 755; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 828 ATGAAAAACAATAAAGATATTGAAGAAAAATGTTATTTTGTGTTTGTGACATTTCTT 887  
DB 1 ATGAAAAACAATAAAGATATTGAAGAAAAATGTTATTTTGTGTTTGTGACATTTCTT 60  
QY 888 GGAATCAATCTCGAAGAGGATTTGCTCAACAGACCCGATCCAGGCAACTTCAC 947  
DB 61 GGAATCAATCTCGAAGAGGATTTGCTCAACAGACCCGATCCAGGCAACTTCAC 120  
QY 948 AGATCTAGTTTGTGTTAAAAACCTTCAAAATATATATTTTCTTATGAGGGTGACCTGTT 1007  
DB 121 AGATCTAGTTTGTGTTAAAAACCTTCAAAATATATATTTTCTTATGAGGGTGACCTGTT 180  
QY 1008 ACTCAGAGATGTGAATCTGTGATCAACTTTTATCTCACAATTTATATATATATGTT 1067  
DB 181 ACTCAGAGATGTGAATCTGTGATCAACTTTTATCTCACAATTTATATATATATGTT 240  
QY 1068 TCAGGGCCAAATATGATAAATTAATAAAGCTGAACCTTAAGAACCAAGAGATGCCACTTTA 1127  
DB 241 TCAGGGCCAAATATGATAAATTAATAAAGCTGAACCTTAAGAACCAAGAGATGCCACTTTA 300  
QY 1128 TTTAAGGATAAAACCTTGATATTTATGGTGTAGATATTTACCATCTCTGTTTATTATGT 1187  
DB 301 TTTAAGGATAAAACCTTGATATTTATGGTGTAGATATTTACCATCTCTGTTTATTATGT 360  
QY 1188 GAAATGCGAAGAGGATGATCTATCTACGGGGGTAAACATCATGAAGGATCAT 1247  
DB 361 GAAATGCGAAGAGGATGATCTATCTACGGGGGTAAACATCATGAAGGATCAT 420  
QY 1248 TTAGAATTCCTTAAAAAGATAGTCGTTTAAAGTATCAATCGATGGTATCAAAAGCCTATCA 1307  
DB 421 TTAGAATTCCTTAAAAAGATAGTCGTTTAAAGTATCAATCGATGGTATCAAAAGCCTATCA 480  
QY 1308 TTTGATATTGAACAAATAAATAAATGTTAACTGCTCAAGATTTAGACTATAAAGTTAGA 1367  
DB 481 TTTGATATTGAACAAATAAATAAATGTTAACTGCTCAAGATTTAGACTATAAAGTTAGA 540  
QY 1368 AAATATCTTACAGATAAAGCAATATATATCTAATGGACCTTCTAAATGAACACTGA 1427  
DB 541 AAATATCTTACAGATAAAGCAATATATATCTAATGGACCTTCTAAATGAACACTGA 600  
QY 1428 TATATAAGTTTCACTAAGATAAAGAAAGTTTGTGTTGTTGTTTCCCTGAACCA 1487  
DB 601 TATATAAGTTTCACTAAGATAAAGAAAGTTTGTGTTGTTGTTTCCCTGAACCA 660  
QY 1488 GAATTTTACTCAATCTAAATATCTTATGATATATAAGATAAAGAAAGCTTGCACCAAC 1547  
DB 661 GAATTTTACTCAATCTAAATATCTTATGATATATAAGATAAAGAAAGCTTGCACCAAC 720  
QY 1548 ACAAGCCAAATTGAATCTACCTTAAACCAACCAAGTAA 1583  
DB 721 ACAAGCCAAATTGAATCTACCTTAAACCAACCAAGTAA 756

RESULT 12  
ACD28908

ID ACD28908 standard; DNA; 1419 BP.

XX AC ACD28908;

DT 27-AUG-2003 (first entry)

XX SPEa L42R/SPEb C47S mutant fusion protein, DNA.

XX SPEa; streptococcus pyrogenic enterotoxin; gene; mutant; vaccine; ds;

KW superantigen toxin; MHC; superantigen-associated bacterial infection;  
KW bacterial infection; antibacterial; SPEb.  
OS Streptococcus sp.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT 1. 1419  
FT /\*tag= a  
FT /product= "SPEa L42R/SPEb C47S"  
FT /transl\_except= (pos:298. 306,aa:Ile-Gly)  
FT /transl\_except= (pos:634. 642,aa:Thr-Gln)  
FT /transl\_except= (pos:1162. 1170,aa:Ser-Gln)  
FT /transl\_except= (pos:1228. 1236,aa:Gly-Gly)  
PN US2003036644-A1.  
XX 20-FEB-2003.  
XX 26-NOV-2001; 2001US-00002784.  
XX 25-JUN-1997; 97US-00882431.  
PR 01-SEP-1998; 98US-00144776.  
XX (ULRI/) ULRICH R G.  
PI ULRICH RG;  
XX WPI; 2003-492125/46.  
DR P-PSDB; ABU62335.  
XX New superantigen toxin DNA fragment, useful for preparing a composition  
PT for treating or preventing bacterial infection.  
XX Claim 6; Page 39-40; 68pp; English.  
XX The invention relates to an isolated and purified superantigen toxin DNA  
CC fragment is altered so that binding of the encoded altered toxin to  
CC either the MHC class II or T cell antigen receptor is altered. Also  
CC included are a recombinant DNA construct (comprising a vector and an  
CC isolated and purified altered superantigen toxin DNA fragment), a host  
CC cell transformed with the recombinant DNA construct, producing altered  
CC superantigen toxin, an altered TSS-1 (toxic shock syndrome toxin)  
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial  
CC infection, a vaccine (comprising an altered superantigen toxin for  
CC producing antigenic and immunogenic response resulting in the protection  
CC of a mammal against superantigen-associated bacterial infection),  
CC treating/ameliorating a superantigen-associated bacterial infection, an  
CC antisera isolated from individuals immunised with one or more altered  
CC TSS-1 superantigen toxin and an antibody which recognises altered TSS-  
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,  
CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and  
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a  
CC composition for treating or preventing bacterial infection. The present  
CC sequence encodes the SPEa L42R/SPEb C47S mutant fusion protein  
XX Sequence 1419 BP; 497 A; 266 C; 255 G; 401 T; 0 U; 0 Other;

Query Match 35.5%; Score 656.8; DB 8; Length 1419;  
Best Local Similarity 94.2%; Pred. No. 7e-97;  
Matches 682; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 918 CAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 977  
DB 4 CAACAGACCCCGATCCAGCCAACTTCACAGATCTAGTTAGTTAAACCTTCAAAAT 63  
QY 978 ATATATTTCTTTATGAGGGTGACCTGTTACTCAGAGATGGAATCTGTTGATCAA 1037  
DB 64 ATATATTTCTTTATGAGGGTGACCTGTTACTCAGAGATGGAATCTGTTGATCAA 123  
QY 1038 CTTTATCTCAACATTTAATATAATGTTTCAGGGCCAAATTTATGATAAATTTAAACT 1097  
DB 124 CTTGATCTCAGATTTAATATAATGTTTCAGGGCCAAATTTATGATAAATTTAAACT 183



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Db 664 AACGACCAAGTGTGTTAAATCTCTCTTGATTCAAAGGCAATTCATTACAAATCAAGGTAC 723
QY 1638 TCTT 1641
Db 724 CCTT 727

RESULT 14
ACA64721
ID ACA64721 standard; DNA; 1497 BP.
XX
AC ACA64721;
XX
DT 18-JUN-2003 (first entry)
XX
DE Staphylococcus/Streptococcus erythrogenic toxin gene.
XX
KW Superantigen; ds; gene; SAG; staphylococcal enterotoxin; tumour; cancer;
KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;
KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
KW tumouricidal immunocyte; antitumour.
XX
OS Staphylococcus sp.
OS Streptococcus sp.
XX
PN US2002177551-A.
XX
PD 28-NOV-2002.
XX
PF 30-MAY-2001; 2004US-00870759.
XX
PR 31-MAY-2000; 2004US-0208128P.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS.
XX
WPI; 2003-361759/34.
DR P-PSDB; ABU79113.
XX
PT A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumor associated lipids where the binding induces anergy or apoptosis
PT in T cells and antigen presenting cells.
XX
PS Example 2; Page; 167pp; English.
XX
CC The invention relates to a mammalian cell receptor, useful in the
CC treatment of cancer, which binds to tumour associated lipids and induces
CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
CC Also included are a mammalian cell useful in the treatment of cancer
CC where the receptor which binds tumour associated lipids and induces
CC cellular inactivation or death is deleted or functionally deactivated,
CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
CC (by allowing tumour associated lipids to contact immunocytes in which
CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
CC deleted), a construct useful in the treatment of cancer comprising a
CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
CC useful in the treatment of cancer (where an adaptor protein which
CC inhibits T cell activation by tumour associated antigens is deleted or
CC functionally deactivated), a composition useful in the treatment of
CC cancer (comprising a lipid raft conjugated to a superantigen), producing
CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
CC allowing tumour associated lipids to contact immunocytes, in which
CC receptors for the lipids are inactivated or deleted to produce a
CC tumouricidal immunocyte population, and administering the tumouricidal
CC activated immunocytes to the host), producing (M3) a tumouricidal APC
CC population ex vivo in a mammal (by allowing a tumour associated lipid to
CC contact APCs, in which receptors for the tumour associated lipids are
CC inactivated or deleted to produce a tumouricidal activated population,
CC and administering APCs to the host), producing a tumouricidal T cell
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CC population ex vivo in a mammal) by allowing a tumour associated lipids to
CC contact T cells, in which adaptor proteins, which inhibit T cell
CC activation by tumour associated antigens, are deleted or functionally
CC deactivated to produce a tumouricidal population of T cells, and
CC administering the tumouricidally activated T cells to the host, or
CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC administering the tumouricidally activated T cells to the host), treating
CC (M5) cancer in a mammal (by administering a lipid binding molecule which
CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC a tumouricidal T cell population in vivo in a mammal (by allowing a
CC tumour associated antigen to contact immunocytes in which adaptor
CC proteins which inhibit T cell activation by tumour associated antigens
CC are deleted or functionally deactivated) and producing (M7) a
CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC receptors, methods and compositions are useful for treating cancers and
CC tumours. Bacterial superantigens are co-administered or administered as
CC fusion constructs with anti-tumour proteins or motifs. The present
CC sequence encodes an anti-tumour protein which is co-administered with or
CC incorporated into a fusion construct with a superantigen. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from the US patent
CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX
SQ Sequence 1497 BP; 584 A; 247 C; 246 G; 420 T; 0 U; 0 Other;

Query Match 15.0%; Score 278; DB 7; Length 1497;
Best Local Similarity 99.7%; Pred. No. 6.5e-36;
Matches 289; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 40 AAGCTTACTTTTCGAATCAGGTCTATCTCTTGAACAGGTGCAACATAGATTAGGCGATGG 99
Db 1209 AAGCTTACTTTTCGAATCAGGTCTATCTCTTGAACAGGTGCAACATAGATTAGGCGATGG 1268
QY 100 AGATTACACAGCAACTATGAACGTATATCTATCTATCTATCAATCGCAATCGCAATGATGACA 159
Db 1269 AGATTACACAGCAACTATGAACGTATATCTATCTATCTATCAATCGCAATCGCAATGATGACA 1327
QY 160 TTGGAACCTAAATTCATCAATTTGTTTACTTAAACAGCACTAGATTGACAACTAATTCTCA 219
Db 1328 TTGGAACCTAAATTCATCAATTTGTTTACTTAAACAGCACTAGATTGACAACTAATTCTCA 1387
QY 220 ACAACAGTTAATTTAAACAACATTCAGTAATTCACCAAGTCCCAAGTCCCAATGCTTACCGTA 279
Db 1388 ACAACAGTTAATTTAAACAACATTCAGTAATTCACCAAGTCCCAAGTCCCAATGCTTACCGTA 1447
QY 280 AGTAATCATTAATCTTACTTAAACCTTGTGTACATCAAGGTTTTTTCTTTTGG 329
Db 1448 AGTAATCATTAATCTTACTTAAACCTTGTGTACATCAAGGTTTTTTCTTTTGG 1497

RESULT 15
AAZ51107
ID AAZ51107 standard; DNA; 1712 BP.
XX
AC AAZ51107;
XX
DT 05-JUN-2000 (first entry)
XX
DE Staphylococcal enterotoxin B encoding DNA.
XX
KW Superantigen toxin; SAG; Staphylococcal enterotoxin B; SEB; cytostatic;
KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
KW antibody; toxoid; Staphylococcal/streptococcal toxin; diagnosis;
KW treatment; superantigen-associated bacterial infection; ds.
XX
OS Staphylococcus sp.
XX
FH Key Location/Qualifiers
FT CDS 244..1044
FT /*tag= a
FT /product= "Staphylococcal enterotoxin B"
FT sig_peptide 247..327
```



FT mat\_peptide /\*tag= b  
328..1041  
/\*tag= c  
/label= Mature Staphylococcal enterotoxin B  
/note= "Also includes the ATG start codon"  
/transl\_except= (pos:772..774, aa:Tyr)  
/transl\_except= (pos:901..903, aa:Gln)  
/transl\_except= (pos:904..909, aa:Asn)  
/transl\_except= (pos:1012..1014, aa:Leu)

XX WO200009154-A1.  
XX PD 24-FEB-2000.  
XX PF 13-AUG-1998; 98WO-US016766.  
XX PF 13-AUG-1998; 98WO-US016766.  
XX PR (REED-) REED ARMY INST RES WALTER.  
XX PA Ulrich RG, Olson MA, Bavari S;  
XX PI WPI: 2000-224177/19.  
XX DR P-FSDB; AAY70104.  
XX

Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections.

Claim 4; Page 76-77; 118pp; English.

The present sequence is the DNA encoding Staphylococcal enterotoxin B (SEB), a bacterial superantigen toxin (Sag). The coding region of the Sag toxin when altered by site directed mutagenesis, results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SEB has antibacterial and cytostatic activity. This sequence is useful for the production of SEB vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated bacterial infections

Sequence 1712 BP; 596 A; 223 C; 255 G; 638 T; 0 U; 0 Other;

Query Match 10.0%; Score 184.2; DB 3; Length 1712;  
Best Local Similarity 54.5%; Pred. No. 8.1e-21;  
Matches 552; Conservative 0; Mismatches 408; Indels 53; Gaps 7;

621 ACCTATCTATTCGTAAGATAAATAAATACTATTGTTTTTTTTTTGTTTATTTATAATAAA 680  
29 AACACTATGTTGTTAAAGATGTTTCGTATATAAGTTAGGTGATGATAGTTACTTAAT 88  
681 ATTATTATATAAGTTAATGTTTTTTTAAATAATACAAATTTATCTATTATAGTTAGC 740  
89 TTTAAAGCATAACTTAATTAATATAATAAATACATGAGATTATTAATAATAATTAAGTTTC 148  
741 TATTTTTTTCATTTGTTAGTAATATCGTGAATTTGTAATAACCTTTTAAATCTAGAGGAGA 800  
149 TTTTATGTTTTTTTAAATGATATTTAAGATTTAAGATTTAACAATATTTAAGTGTATCTAGA 208  
801 ACCGAGATATAAA--ATGAGGAGATTAATATGGGAAAAACAATAAAAGATTTGAAGAAAA 858  
209 TACTTTTTGGGAATGTTGGATAAAGAGATAAAAAAATGTATAAGAGATTATTTATTTCCAC 268  
859 TGGTATTTTTTTGTTTT--AGTGACATTTCTTTGGACTAACATCTCGCAAGAGGTTATTG 915  
269 ATGTAATTTGATATTCGCACCTGATATTAGTTATTCTACACCCAAACGTTTTAGCAGAGA 328  
916 CTCACACAGACCCCGATCCAAAGCCAACTTCAAGATCTAGTTAGTTAA--AAACCTTC 972  
329 GTCAACACAGATCTAAACACAGATGAGTTGCAAAATTCGAGTAAATTCACCTGGTTGATGG 388  
973 AAAATATATATTTCTTTTATAGGGTGACCTGTTACTCACGAGATGTGAATCTGTTG 1032

Db 389 AAGATATGAAGCTTTTGTATGATGATAATCATGTATCAGCAATAAACGTTAAATCTATAG 448  
Qy 1033 ATCAACTTTTATCTCACCATTAAATATATATGTTTTCAGGGCCAA-----ATTATG 1083  
Db 449 ATCAATTTCTATACATTGACITTAATATATTTTATTAAGACACTAAGTTAGGGGATTAG 508  
Qy 1084 ATAAATTAATAAACTGAACCTTAAGAACCAAGAGATGCGCAACTTTATTTAAGGATAAAAAACG 1143  
Db 509 ATAAATGTTGAGTCGAATTTTAAACCAAAAGATTTAGCTGATATAATACAAAGATAAATACG 568  
Qy 1144 TTGATATTTATGTTGATAGATATTTACCATCTCTGTTATTTATGTCGAAA----- 1192  
Db 569 TAGATGTTGTTGAGCTAATTTATTTATCAATGTTATTTTCTTAAAAAACAAGATGATA 628  
Qy 1193 -----TGCAGAAAGAGAGTGCTATCTACGGAGGGGTAAACAAATCATG 1236  
Db 629 TTAATTCGCATCAAACTGACAAACGAAAACTTGTATGTATGTTGTTGTTAATCTGAGCATA 688  
Qy 1237 AAGGGAATCATTTAGAAATTCCTAAAAGATAGTGTTHAAGTATCAATCGATGGTATCC 1296  
Db 689 ATGGAACCAATTAGATAAATATAGAAGTATTACTGTTGCGGTATTTGAAGATGGTAAAA 748  
Qy 1297 AAAGCCTATCATTTGATATTGAAACAAATAAAAAAATGTTAACTGCTCAAGAAATTAGACT 1356  
Db 749 ATTTATTTCTTTTGACGTACAACTTAAGAAAAAGTGCTGCTCAAGAAATTAGATT 808  
Qy 1357 ATAAAGTTAGAAAAATCTTTACAGATAATAAGCACTATATACTTAATGGACCTTCTAAAT 1416  
Db 809 ACCTAACTCGTCACTATTTTGGTGAAAAATAAAAAAATCTTATGAATTTAAACAACGCTT 868  
Qy 1417 ATGAAACTGGATATATAAAGTTTCATACCTAAGAATAAAGAAAGTTTTTGGTTTGATTTT 1476  
Db 869 ATGAAACGGGATATATAAATTTATA--GAATGAGATAGCTTTTGGTATGACATGA 925  
Qy 1477 TCCTCGAACCCAG-----AATTTACTCAATCAATATCTTTATGATATATAAGATAATG 1530  
Db 926 TGCCTGCACCGAGAGATAAATTTGCCAATCTAAATATTTAATGATGTACAATGACAATA 985  
Qy 1531 AAACGCTTGACTCAACACACAGCCCAATTTGAAGTCTTACCTAACCAACCAAGTAA 1583  
Db 986 AAATGTTGATTTCTTAAAGATGTGAAGATTGAAGTTTATCTTACGACAAAGAAA 1038

Search completed: May 9, 2004, 13:27:40  
Job time : 706 secs